STIC-Biotech/ChemLib

174430

From:

Dunston, Jennifer

Sent:

Friday, December 16, 2005 8:35 AM

To: Subject:

STIC-Biotech/ChemLib Sequence Search 10/659782

Please search the amino acid sequence of SEQ ID NO: 32 against the commercial nucleic acid databases.

Thank you.

Jennifer Dunston, Ph.D. USPTO Art Unit 1636 REM 2B76 Mailbox: REM 2C70 (571) 272-2916 NECHVED

Searcher:
Searcher Phone:
Date Searcher Picked up:
Date completed:

Date completed:
Online Time:
Online Time:

Type of Search

NA#______ AA#:____

S/L:_____ Oligomer:_____

Encode/Transl:_____ Text:____

Structure #:_____ Text:____

Inventor:_____ Litigation:____

Vendors and cost where applicable
STN:_____
DIALOG:___
QUESTEL/ORBIT:___
LEXIS/NEXIS:___
SEQUENCE SYSTEM:__
WWW/Internet:__
Other (Specify):____

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Sequence 3, Application US/10294191A

Sequence 3, Application No. US20030211512A1

GENERAL INFORMATION:
APPLICANT: Rochschild, Max F.
APPLICANT: Rim, Kwan Suk
APPLICANT: Kim, Kwan Suk
APPLICANT: EXPERENCE: P05408031

CURRENT APPLICATION NUMBER: US/10/294,191A

CURRENT PILING DATE: 2002-11-14

PRIOR APPLICATION NUMBER: US 60/333,222

PRIOR FILING DATE: 2001-11-14

NUMBER OF SEQ 1D NOS: 16

SOFTWARE: Patentin version 3.1

SEQ 1D NO 3
                                                                                                                                                                                                                                                                                                                           US-10-659-782A-32
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Sequence 2, Appli
Sequence 2, Appli
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                                                                             December 21, 2005, 13:36:08; Search time 164 Seconds (without alignments) 298.086 Million cell updates/sec
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1 MPSPGTVCSLLLLGMLWLDL......PPSSRERSRRSHQPSCSPEL 117
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
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Compugen Ltd.
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US-10-294-191A-3
US-10-474-191A-3
US-00-194-987-2
US-09-883-722-268
US-09-989-723-268
US-09-989-723-268
US-09-989-721-268
US-09-989-731-268
US-09-991-073-268
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US-09-991-163-268
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                                                                                                                                                                                                                                           1867569 seqs, 417829326 residues
GenCore version (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Search

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APPLICANT: Mintz, Liat
TITLE OF INVENTION: Compositions, Reagents and Kits for and Methods of Diagnosing,
TITLE OF INVENTION: Monitoring and Treating Obesity and/or Diabetes
FILE REFERENCE: 28238
CURRENT APPLICATION NUMBER: US/10/659,782A
CURRENT FILING DATE: 2003-09-11
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin version 3.2
SEQ ID NO 32
LENGTH: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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  61 QORHLWASVFSQSTKDSGSDLTVSGRTWGLRVLNRLFPPSSRERSRRSHQPSCSPEL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 QORH-WASVFSQSTKDSGSDLTVSGRTWGLRVLNRLFPPSSRERSRRSHQPSCSPEL 116
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Sequence
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Pred. No. 1.1e-57;
0; Mismatches 0; Indels 1;
US-09-989-724-268
US-09-989-728-268
US-09-993-647-268
US-09-997-428-268
US-09-997-428-268
US-09-990-438-268
US-09-990-711-268
US-09-998-156-268
US-09-998-156-268
US-09-991-157-268
US-09-997-573-268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 32, Application US/10659782A Publication No. US20050059015A1 GENERAL INFORMATION:
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Best Local Similarity 99.1%;
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
US-10-659-782A-32
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31.9%; Score 198; DB 3; Length 117; 88.6%; Pred. No. 2e-13; tive 0; Mismatches 5; Indels
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31.9%; Score 198; DB 3;
Best Local Similarity 88.6%; Pred. No. 2e-13;
Matches 39; Conservative 0; Mismatches
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Sequence 2, Application US/09853253
Patent No. US20020055156A1
GENERAL INFORMATION:
APPLICANT: SHEPPARD, FAUL
APPLICANT: BISPRENCE, FAUL
APPLICANT: BISHOF, PAUL
TILE OF INVENTION: Zsig33-like Peptides
FILE REFERENCE: 00-30
CURRENT APPLICATION NUMBER: US/09/853,253
CURRENT APPLICATION NUMBER: 06/203,300
PRIOR FILING DATE: 2000-05-11
PRIOR FILING DATE: 2000-05-11
NUMBER OF SEO ID NOS: 28
SEQ ID NOS: 28
SEQ ID NOS: 28
                                     ATTORNEY/AGENT INFORMATION:
NAME: SAWislak, Deborah
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 97-04
TELEPONNUNICATION INFORMATION:
TELEPONE 206-442-6672
TELEPONE: 206-442-6673
TELEX: <UNKNOWN:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: incernal

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-794-987-2
                      APPLICATION NUMBER: 09/046,479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 268, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bettein, David
; APPLICANT: Bettein, David
; APPLICANT: Eaton, David
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39; Conservative
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, ORGANISM: Homo sapiens
US-09-853-253-2
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Matches 39; Conserva
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US-09-989-722-268
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Sequence 2. Application US/10477506

Sublication No. US20040157227A1

GENERAL INFORMATION:

APPLICANT: Chopin, Lisa K

APPLICANT: Jeffery, Penelope L

APPLICANT: Herington, Adrian C

TILLE OF INVENTION: REPRODUCTIVE CANCER DIAGNOSIS AND THERAPY
FILE REFERENCE: 225.81

CURRENT APPLICATION NUMBER: US/10/477,506

CURRENT APPLICATION NUMBER: PR9567

PRIOR PILING DATE: 2003-11-10

PRIOR PLING DATE: 2001-12-17

PRIOR PLING DATE: 2001-12-17

PRIOR PLING DATE: 2001-12-17

PRIOR APPLICATION NUMBER: PT/AU02/000582

PRIOR FILING DATE: 2002-05-10

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin version 3.1

SEQ ID NO 2

LENGTH: 91
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                                                                                             Query Match 31.9%; Score 198; DB 4; Length 60; Best Local Similarity 88.6%; Pred. No. 9e-14; Matches 39; Conservative 0; Mismatches 5; Indels
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COUNTRY: USA
ZIP: 94102
COMPUTRY: USA
ED104
MEDIUM TYPE: Diskette
COMPUTR: IBM COMPATLALE
OPERATING SYSTEM: DOS
SOFTWARE: FASESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/794,987
FILING DATE: 27-FEb-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                              1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHORVQVRPPHKAP
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88.6%; Pred. No. 1.5e-13;
vative 0; Mismatches 5
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Sequence 2, Application US/09794987

SEQUENCE 2, Application US/09794987

SEQUENCE 3, APPLICANTION OF THE OF INVENTION: MOTILIN HOMOLOGS

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

SADDRESSEE ZYMOGENETICS, INC.

STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 31.9
Best Local Similarity 88.6
Matches 39; Conservative
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US-10-477-506-2
  ; TYPE: PRT
; ORGANISM: Human
US-10-294-191A-3
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R APPLICATION NUMBER: 60/090349
R FILING DATE: 1998-06-23
R FILING DATE: 1998-06-23
R FILING DATE: 1998-06-23
R APPLICATION NUMBER: 60/090429
R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090431
R APPLICATION NUMBER: 60/090431
R APPLICATION NUMBER: 60/090435
R APPLICATION NUMBER: 60/090435
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R APPLICATION NUMBER: 60/089908
R FILING DATE: 1998-06-18
R APPLICATION NUMBER: 60/089947
R FILING DATE: 1998-06-19
R APPLICATION NUMBER: 60/089948
R APPLICATION NUMBER: 60/089948
R APPLICATION NUMBER: 60/089952
R FILING DATE: 1998-06-19
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R FILING DATE: 1998-06-22
R APPLICATION NUMBER: 60/090252
R PILING DATE: 1998-06-22
R APPLICATION NUMBER: 60/090254
R FILING DATE: 1998-06-22
           R APPLICATION NUMBER: 60/088217
R FILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/088655
R APPLICATION NUMBER: 60/088734
R APPLICATION NUMBER: 60/088738
R APPLICATION NUMBER: 60/08878
                                                                                                                                                                                                                                                                                                                                                      R PILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088826
R PILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088851
R PILING DATE: 1998-06-11
R PILING DATE: 1998-06-11
R PILING DATE: 1998-06-11
R PILING DATE: 1998-06-11
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APPLICATION NUMBER: 60/089514
FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089532
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APPLICATION NUMBER: 60/089440
FILING DATE: 1998-06-16
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APPLICATION NUMBER: 60/089599
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089600
FILING DATE: 1998-06-17
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APPLICATION WNDAER: 60/088810
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088824
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APPLICATION NUMBER: 60/089105
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APPLICATION NUMBER: 60/089538
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PPLICATION NUMBER: 60/089598
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APPLICATION NUMBER: 60/089801
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APPLICATION NUMBER: 60/089907
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APPLICANT: Abang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2130PLG3;
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/06250
PRIOR FILING DATE: 1997-10-17
PRIOR PLING DATE: 1997-11-12
PRIOR PLING DATE: 1997-11-13
PRIOR PLING DATE: 1997-11-13
PRIOR PLING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1999-02-25
PRIOR PLING DATE: 1999-02-25
PRIOR APPLICATION NUMBER: 60/078945
PRIOR PLING DATE: 1999-02-26
PRIOR PLING DATE: 1999-02-26
PRIOR PLING DATE: 1999-03-20
PRIOR PLING DATE: 1999-03-20
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PRIOR PILING DATE: 1998-06-04
PRIOR PELING DATE: 1998-06-04
PRIOR PILING DATE: 1998-06-04
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PRIOR PILING DATE: 1998-06-04
PRIOR PILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR PILING DATE: 1998-06-04
PRIOR PILING DATE: 1998-06-04
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FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088202
FILING DATE: 1998-06-05
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PPLICATION NUMBER: 60/083322
ILING DATE: 1998-04-28
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ILING DATE: 1998-05-07
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LING DATE: 1998-05-28
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FILING DATE: 1998-06-02
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FILING DATE: 1998-06-02
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FILING DATE: 1998-06-03
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FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088026
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APPLICATION NUMBER: 60/088212
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                                                                                                                            Godowski, Paul J.
Grimaldi, J.Christopher
Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A
Tumas, Daniel
Ferrara, Napoleone
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                                                 Gerber, Hanspeter
Gerritsen, Mary E.
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                                                                                                        3oddard, Audrey
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APPLICANT:
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Pred. No. 2e-13;
0; Mismatches
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; Patent No. US20020072092A1
; GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Ferrara, Napoleone
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hangpeter
APPLICANT: Geritsen, Mary E.
                                                                                                       PRIOR FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR APPLICATION NUMBER: 60/090515
PRIOR PLING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PRIOR DATE: 1998-06-24
PRIOR PRIOR DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/09057
PRIOR PRILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/09069
PRIOR PILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/09069
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-07
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Gerriteen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
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88.6%;
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Best Local Similarity 88.6
Matches 39; Conservative
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR PILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-07
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Patent No. US20020072496A1
GENERAL INFORMATION:
APPLICANT: Bakenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Godowвki, Paul J.
Grimaldi, J. Christopher
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Stewart, Timothy A.
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Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
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Pan, James
Paoni, Nicholas F.
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APPLICANT:
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APPLICANT:
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R FILING DATE: 1998-06-11

R APPLICATION NUMBER: 60/089105

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R FILING DATE: 1998-06-12

R APPLICATION NUMBER: 60/089105

R FILING DATE: 1998-06-16

R APPLICATION NUMBER: 60/089513

R FILING DATE: 1998-06-16

R APPLICATION NUMBER: 60/089514

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089538

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089538

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/08959

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/08959

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/08969

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/08999

R FILING DATE: 1998-06-18

R FILING DATE: 1998-06-18

R APPLICATION NUMBER: 60/08999

R FILING DATE: 1998-06-19

R APPLICATION NUMBER: 60/08999

R FILING DATE: 1998-06-19

R APPLICATION NUMBER: 60/08999

R FILING DATE: 1998-06-19

R APPLICATION NUMBER: 60/090254

R FILING DATE: 1998-06-19

R APPLICATION NUMBER: 60/090355

R FILING DATE: 1998-06-22

R APPLICATION NUMBER: 60/090355

R FILING DATE: 1998-06-22

R APPLICATION NUMBER: 60/090435

R FILING DATE: 1998-06-22

R APPLICATION NUMBER: 60/090435

R FILING DATE: 1998-06-23

R APPLICATION NUMBER: 60/090445

R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090445

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APPLICATION NUMBER: 60/090557
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090676
FILING DATE: 1998-06-25
                            APPLICATION NUMBER: 60/088826
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088858
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APPLICATION NUMBER: 60/090540
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090542
   PRIOR 
                                                                                                            APPLICANY: Mood, MILLIAM I. INGO, MILLIAM I. APPLICANY: Mood, MILLIAM I. APPLICANY: Mood, MILLIAM I. MOOD, M
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APPLICATION UNDRER: 60/08810
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/08824
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
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CURRENT APPLICATION NUMBER: US/09/989,727
CURRENT PILLING DATE: 2001-11-9
PRIOR PILLING DATE: 1997-06-16
PRIOR PILLING DATE: 1997-10-17
PRIOR FILLING DATE: 1997-10-17
PRIOR FILLING DATE: 1997-10-17
PRIOR FILLING DATE: 1997-10-17
PRIOR FILLING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065311
PRIOR PILLING DATE: 1997-11-24
PRIOR PILLING DATE: 1997-11-24
PRIOR FILLING DATE: 1998-02-25
PRIOR FILLING DATE: 1998-02-25
PRIOR FILLING DATE: 1998-02-25
PRIOR PILLING DATE: 1998-03-20
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PRIOR PILLING DATE: 1998-03-20
PRIOR PILLING DATE: 1998-03-20
PRIOR PILLING DATE: 1998-04-28
PRIOR PILLING DATE: 1998-04-28
PRIOR PILLING DATE: 1998-04-28
PRIOR PILLING DATE: 1998-04-28
PRIOR PILLING DATE: 1998-06-02
PRIOR PILLING DATE: 1998-06-03
PRIOR PILLING DATE: 1998-06-04
PRIOR PILLING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/08032
PRIOR PILLING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/08033
PRIOR PILLING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/08033
PRIOR PILLING DATE: 1998-06-06-06-06-06-06-06-06-06-
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RAPLICATION NUMBER: 60/078910

RAPLICATION NUMBER: 60/083322

RAPLICATION NUMBER: 60/08400

RAPLICATION NUMBER: 60/08700

RILING DATE: 1998-06-02

RAPLICATION NUMBER: 60/08020

RAPLICATION NUMBER: 60/08030

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APPLICATION NUMBER: 60/08861
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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31.9%; Score 198; DB 3; Length 117;
Best Local Similarity 88.6%; Pred. No. 2e-13;
Matches 39; Conservative 0; Mismatches 5; Indels
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Patent No. US20020072497A1
GENERAL INFORMATION:
APPLICANT: ABKERBAZI, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bottein, David
APPLICANT: Bettein, David
APPLICANT: Eaton, Dan I.
APPLICANT: Forg. Sherman
APPLICANT: Forg. Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
                     PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR PILING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
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PRIOR PILING DATE: 1998-06-26
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PRIOR PELING DATE: 1998-07-01
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PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091519
PRIOR PELING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-07
APPLICATION NUMBER: 60/090678
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Grimaldi, J. Christopher
Gurney, Austin L.
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Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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PRIOR APPLICATION NUMBER: 60/08910
PRIOR PILING DATE: 1998-66-11
PRIOR PILING DATE: 1998-66-12
PRIOR PILING DATE: 1998-66-12
PRIOR PILING DATE: 1998-66-12
PRIOR PILING DATE: 1998-66-16
PRIOR PILING DATE: 1998-66-16
PRIOR PILING DATE: 1998-66-17
PRIOR APPLICATION NUMBER: 60/08531
PRIOR PILING DATE: 1998-66-17
PRIOR APPLICATION NUMBER: 60/08599
PRIOR PAPALCATION NUMBER: 60/08599
PRIOR PAPALCATION NUMBER: 60/08599
PRIOR PAPALCATION NUMBER: 60/08999
PRIOR PILING DATE: 1998-66-17
PRIOR PILING DATE: 1998-66-18
PRIOR
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C70
CURRENT APPLICATION NUMBER: US/09/989,731
CURRENT FILING DATE: 2001-11-20
PRIOR PAPLICATION NUMBER: 60/049787
PRIOR PLING DATE: 1997-706-16
PRIOR PLING DATE: 1997-10-17
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88.6%; Pred. No. 2e-13;
:ive 0; Mismatches
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR PLING DATE: 1998-06-26
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PRIOR PELING DATE: 1998-07-01
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PRIOR PELING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR PELING DATE: 1998-07-07
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Patent No. US20020103125A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Wattanabe, Colin K.
William, P. Mickey
Wood, William I.
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Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
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Best Local Similarity 88.65
Matches 39; Conservative
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Napier, Mary A.
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US-09-989-731-268
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PRIOR APPLICATION NUMBER: 60/089532
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PRIOR APPLICATION NUMBER: 60/090659
PRIOR APPLICATION NUMBER: 60/090659
PRIOR APPLICATION NUMBER: 60/090696
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-06-26

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R APPLICATION NUMBER: 60/088655
R APPLICATION NUMBER: 60/088655
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R FILING DATE: 1998-06-10
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R FILING DATE: 1998-06-10
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R FILING DATE: 1998-05-07
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A APPLICATION NUMBER: 60/088202
R FILING DATE: 1998-06-05
A PILICATION NUMBER: 60/088212
R FILING DATE: 1998-06-05
A APPLICATION NUMBER: 60/088217
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/08826
APPLICATION NUMBER: 60/088858
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APPLICATION NUMBER: 60/088861
FILING DATE: 1998-06-11
FILING DATE: 1998-06-11
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APPLICATION NUMBER: 60/087609
FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087759
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APPLICATION NUMBER: 60/088021
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088025
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APPLICATION NUMBER: 60/088026
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088028
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APPLICATION NUMBER: 60/088029
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088030
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APPLICATION NUMBER: 60/088033
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APPLICATION NUMBER: 60/088326
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088167
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APPLICATION NUMBER: 60/087827
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APPLICANT: Stewart, Timethy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: William I.
APPLICANT: William I.
APPLICANT: Shang, Zemin
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PICS7
CURRENT APPLICATION NUMBER: US/09/989,732
CURRENT PILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/06436
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/065311
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                     PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
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Patent No. US20020123463A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Kevin P.
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Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Gerritsen, Mary E.
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PRIOR FILMS DATE: 1989-0-0-2

PRIOR FILMS DATE: 1989-0-0-1

PRIOR APPLICATION NUMBER: 60/19312

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MBER: 60/087106 998-05-28 MBER: 60/087607 998-06-02 MBER: 60/087609 998-06-02 998-06-02 MBER: 60/087827 998-06-03 MBER: 60/08021 998-06-04	NUMBER: 60/088026 NUMBER: 60/088028 NUMBER: 60/088029 1998-06-04 NUMBER: 60/088030 1998-06-04 NUMBER: 60/088033 1998-06-04 NUMBER: 60/088033 1998-06-04 NUMBER: 60/088126 1998-06-05 NUMBER: 60/08812 1998-06-05 NUMBER: 60/08812 1998-06-05 NUMBER: 60/08812 1998-06-05 NUMBER: 60/08812 1998-06-05 NUMBER: 60/088136 1998-06-05 NUMBER: 60/088136 1998-06-09 NUMBER: 60/088136 1998-06-10 NUMBER: 60/08810	60000000000000000000000000000000000000
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PRIOR FILING DATE: 1998-06-18

PRIOR APPLICATION NUBBER: 60/08901

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PRIOR PLILICATION NUBBER: 60/08908

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PRIOR PLILICATION NUBBER: 60/08025

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PRIOR PLILICATION NUBBER: 60/090616

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R APPLICATION NUMBER: 60/088217
R FILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/088217
R FILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/088655
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R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088742
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R FILING DATE: 1998-06-11
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R FILING DATE: 1998-06-17
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R APPLICATION NUMBER: 60/089599
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089599
R FILING DATE: 1998-06-17
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R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089601
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                         R APPLICATION NUMBER: 60/087827

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R APPLICATION NUMBER: 60/088021

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R APPLICATION NUMBER: 60/088025

R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088030

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R APPLICATION NUMBER: 60/088167
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FILING DATE: 1998-06-18
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FILING DATE: 1998-06-18
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APPLICATION NUMBER: 60/088212
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CURRENT APPLICATION WHORER: US/09/990,442
CURRENT APPLICATION WHORER: 00/049787
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION WHORER: 60/06250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION WHORER: 60/06310
PRIOR APPLICATION WHORER: 60/06310
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION WHORER: 60/06311
PRIOR APPLICATION WHORER: 60/06310
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PRIOR FILING DATE: 1998-06-03
PRIOR PRILING DATE: 1998-06-03
PRIOR PRILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/08759
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31.9%; Score 198; DB 3; Length 117;
Best Local Similarity 88.6%; Pred. No. 2e-13;
Matches 39; Conservative 0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 268, Application US/09990442
Patent No. US20020132252A1
GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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Grimaldi, J. Christopher
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
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Goddard, Audrey
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Kljavin, Ivar J.
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0; Gaps

5; Indels

0, Mismatches

39; Conservative

Matches

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PRIOR FILING DATE: 1938-06-19
PRIOR PAPLICATION NUMBER: 60/08952
PRIOR PAPLICATION NUMBER: 60/08952
PRIOR FILING DATE: 1938-06-19
PRIOR FILING DATE: 1938-06-29
PRIOR FILING DATE: 1938-06-22
PRIOR PLING DATE: 1938-06-22
PRIOR PLING DATE: 1938-06-22
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PRIOR APPLICATION NUMBER: 60/09049
PRIOR PLING DATE: 1938-06-23
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PRIOR PRILING DATE: 1938-06-24
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PRIOR PRILING DATE: 1938-06-25
PRIOR PRILING DATE: 1938-06-26
PRIOR PRILING DATE: 1938-07-01
PRIOR PRILING DATE: 1938
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Score 198; DB 3; Length 117; Pred. No. 2e-13;

31.9%; 88.6%;

Query Match Best Local Similarity

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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P23091C17
CURRENT APPLICATION WUMBER: US/09/991,163
CURRENT APPLICATION WUMBER: 06/049787
PRIOR PLILING DATE: 2001-11-14
PRIOR FILING DATE: 1997-10-17
PRIOR PELLING DATE: 1997-10-17
PRIOR PELLING DATE: 1997-10-17
PRIOR APPLICATION WUMBER: 60/065311
PRIOR PLILING DATE: 1997-10-17
PRIOR APPLICATION WUMBER: 60/065312
PRIOR PLILING DATE: 1997-10-17
PRIOR PLILING DATE: 1997-10-17
PRIOR PLILING DATE: 1998-03-20
PRIOR PLILING DATE: 1998-06-02
PRIOR PLILING DATE: 1998-06-03
PRIOR PLILING DATE: 1998-06-03
PRIOR PLILING DATE: 1998-06-03
PRIOR PLILING DATE: 1998-06-03
PRIOR PLING DATE: 1998-06-03
                                   1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 44
                                                                                                                                                                                                                          Sequence 268, Application US/09991163
Patent No. US20020132253A1
GENERAL INFORMATION:
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Grimaldi, J. Christopher
Gurney, Austin L.
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Stewart, Timothy A.
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Gerritsen, Mary E.
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Botstein, David
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Pan, James
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PRIOR APPLICATION NUMBERS: 60/08020
PRIOR APPLICATION NUMBERS: 60/08020
PRIOR APPLICATION NUMBERS: 60/08021
PRIOR PLINKO DATE: 1998-06-04
PRIOR PLINKO DATE: 1998-06-04
PRIOR PLINKO DATE: 1998-06-04
PRIOR PLINKO DATE: 1998-06-05
PRIOR APPLICATION NUMBERS: 60/08021
PRIOR PRIOR CONTROL NUMBERS: 60/08021
PRIOR PRIOR DATE: 1998-06-05
PRIOR PRIOR DATE: 1998-06-10
PRIOR PRIOR PRIOR DATE: 1998-06-11
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| PRIOR PLING DATE: 1998 - 66-25
| PRIOR PLING DATE: 1998 - 66-24
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R FILING DATE: 1998-06-12

R APPLICATION NUMBER: 60/089440

R FILING DATE: 1998-06-16

R APPLICATION NUMBER: 60/089512

R APPLICATION NUMBER: 60/089514

R APPLICATION NUMBER: 60/089514

R APPLICATION NUMBER: 60/089514

R APPLICATION NUMBER: 60/089518

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/08959

R FILING DATE: 1998-06-17

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R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089600

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089601

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089601

R FILING DATE: 1998-06-18

R APPLICATION NUMBER: 60/089601

R FILING DATE: 1998-06-18

R APPLICATION NUMBER: 60/089901

R RILING DATE: 1998-06-18

R APPLICATION NUMBER: 60/089901

R RILING DATE: 1998-06-18

R APPLICATION NUMBER: 60/089908

R APPLICATION NUMBER: 60/089908
                           R APPLICATION NUMBER: 60/088033
R FILING DATE: 1998-66-04
R FILING DATE: 1998-66-04
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R APPLICATION NUMBER: 60/088167
R APPLICATION NUMBER: 60/088167
R FILING DATE: 1998-06-05
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R APPLICATION NUMBER: 60/089738
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R FILING DATE: 1998-06-10
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R FILING DATE: 1998-06-11
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FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089952
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APPLICATION NUMBER: 60/090254
FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090349
FILING DATE: 1998-06-23
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FILING DATE: 1998-06-09
APPLICATION NUMBER: 60/088734
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FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/089105
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APPLICATION NUMBER: 60/090246
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APPLICATION NUMBER: 60/090252
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         PRIOR 
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APPLICANT: Zhang, Zemin 1.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acide Encoding the Same TITLE OF INVENTION: Acide Encoding the Same CURRENT PILING INDER: US/09/993,604

CURRENT PILING DATE: 2001-11-14

PRIOR PPLICATION NUMBER: 60/06256

PRIOR PILING DATE: 1997-06-16

PRIOR PILING DATE: 1997-10-17

PRIOR PILING DATE: 1997-11-12

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PRIOR PILING DATE: 1997-11-24

PRIOR PILING DATE: 1997-11-24

PRIOR PILING DATE: 1998-02-25

PRIOR PILING DATE: 1998-03-20

PRIOR PILING DATE: 1998-03-20
RESULT 15
US-09-993-604-268
; Sequence 268, Application US/09993604
; Patent No. US20020137075A1
; GENERAL INFORMATION:
; APPLICANT: Bahkenaai,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
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PRIOR APPLICATION NUMBER: 60/0878759
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PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
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PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
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Godowski, Paul J.
Grimaldi, J.Christopher
Gurney, Austin L.
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Stewart, Timothy A.
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Pan, James
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Eaton, Dan L.
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PRIOR FILING DATE: 1998-06-25
PRIOR PRILING DATE: 1998-07-02
PRIOR PRILING DATE: 1998-07-07
PRIOR PRILING DATE: 199
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Search completed: December 21, 2005, 13:44:36 Job time : 166 secs

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Aaw87991 Protein d
Aay87236 Human sig
Aab20101 Zeig33 pr
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Maximum Match 100%
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AB025061	ABU58977	ABU92355 .	AAE33409	ABU59420	ABU67066	ABU92186	ABU10892	ABU81644	ABU88583	ABO34097	ADA45961	ADA76392	ADA19042	ADA61665	ADB19450	ADB27991	ADA86470	ADB16034	ADA37779	ADA47820
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31.9	31.9	31.9	31.9	31.9	31.9	31.9	31.9	31.9	31.9	31.9	31.9	31.9	31.9	31.9	31.9	31.9	31.9	31.9	31.9	31.9
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'n	9	7.	28	6	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Diagnosis, obesity; anorectic; nutritional disorder; diabetes; antidiabetic; endocrine disease; metabolic disorder; gastrointestinal disease; drug screening; gene therapy; ghrelin. Human ghrelin variant 2 protein, SEQ ID NO: 32 Location/Qualifiers ADY78074 standard; protein; 116 AA. (first entry) Homo sapiens. 02-JUN-2005

/note= "Encoded by CATCTCTGG" Misc-difference

11-SEP-2003; 2003US-00659782. 11-SEP-2003; 2003US-00659782. 17-MAR-2005

WPI; 2005-240894/25. N-PSDB; ADY78053.

New isolated nucleic acid and encoded amino acid sequences useful for diagnosing, monitoring and treating obesity and/or diabetes, or in drug screening purposes.

Claim 32; SEQ ID NO 32; 74pp; English.

The invention relates to alternative splice variants of the obesity and/or diabetes related genes and their corresponding proteins. The invention also relates to compositions, reagents, kits and methods for diagnosing, monitoring and treating obesity and/or diabetes. The composition and methods are useful for diagnosing, monitoring and treating obesity and/or diabetes. These may also be used in drug

1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP

MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP

us-10-659-782b-32.rag

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a method of screening animals to determine those more likely to produce desired growth, appetite and fatness which involves obtaining a sample of genetic material from the animal and assaying for the presence of a genotype in the animal which is associated with favourable growth, appetite and fatness, the genotype characterised by a polymorphism in the ghrelin gene. The composition and methods are useful in screening animals (i.e. pigs) to determine those more or less likely to produce desired growth, appetite and fatness to optimise breeding and selection techniques. The present sequence is human ghrelin protein of the invention.
                                                                                              1,
screening purposes and in gene therapy. The present sequence is the human ghrelin (GHRL) variant protein. This protein is encoded by an obesity and diabetes related gene.
                                                                                                                                   1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAPHVVPALPLSNQLCDLE 60
                                                                                                                    1 MPSPCTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAPHVVPALPLSNQLCDLE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Screening animals (i.e. pigs) to determine those more likely to produce desired growth, appetite and fatness to optimize breeding and selection techniques comprises detecting the presence of a polymorphism in the
                                                                                                                                                                   61 QORHLWASVFSQSTKDSGSDLTVSGRTWGLRVLNRLPPPSSRERSRRSHQPSCSPEL 117
                                                                                                                                                                               QQRH-WASVFSQSTKDSGSDLTVSGRTWGLRVLNRLFPPSSRERSRRSHQPSCSPEL 116
                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                             Growth; appetite; fatness; genotype; polymorphism; ghrelin protein;
breeding; human.
                                                                                                1;
                                                                       Length 116;
                                                                                              Indels
                                                                      Score 605.5; DB 9;
Pred. No. 8.3e-61;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 3; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anderson LL;
                                                                                                                                                                                                                                                    Ź
                                                                                                                                                                                                                                                    ADK66754 standard; protein; 60
                                                                       97.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-NOV-2002; 2002US-00294191.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-NOV-2001; 2001US-0333222P.
                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                     Best Local Similarity 99.1
Matches 116, Conservative
                                                                                                                                                                                                                                                                                                                         Human ghrelin protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ROTH/) ROTHSCHILD M F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rothschild MF, Kim K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (KIMK/) KIM K. (ANDE/) ANDERSON L L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-010667/01.
                                                   Sequence 116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                        US2003211512-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 60 AA;
                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ghrelin gene
                                                                                                                                                                                                                                                                                                 06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                              13-NOV-2003
                                                                                                                                                                                                                                                                          ADK66754;
                                                                         Query Match
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The invention relates to a method for identifying a cancer cell or tissue of the reproductive system by detecting expression of a ghrelin, an exonable deleted preproghrelin and/or a GRIS-R lb proteins or nucleic acids. The antibodies, exon 3-deleted form of preproghrelin and antagonists are useful for treating cancer of the reproductive system such as prostate, ovarian, breast, cervical or uterine cancer, choriocarcinoma or benign prostatic hyperplassia. The present sequence is human exon 3-deleted dhrelin protein
                                                                                                                                                                                                                                                    Ghrelin; preproghrelin; GHS-R 1b; benign prostatic hyperplasia; therapy; breast; cervical; uterine; choriocarcinoma; prostate; ovary; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying a cancer cell or tissue for treating prostate, ovarian, breast cancer, or benign prostatic hyperplasia, by detecting the expression of a ghrelin, an exon-3 deleted preproghrelin and/or a GHS-R 1b proteins or nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 198; DB 6; Length 91;
Pred. No. 2e-14;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chopin LK, Jeffery PL, Herington AC;
                                                                                                                                                                                                      Human exon 3-deleted ghrelin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYQU-) UNIV QUEENSLAND TECHNOLOGY
                                                Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 14; Page 34; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW87991 standard; protein; 117
                                                AAE33410 standard; protein; 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.9%;
88.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-MAY-2001; 2001AU-00004919.
17-DEC-2001; 2001AU-00009567.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-MAY-2002; 2002WO-AU000582
                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-APR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-111957/10.
N-PSDB; AAD50726.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 91 AA;
                                                                                                                                                                                                                                                                                                                                                                                                               40200290387-A1
                                                                                                                                                                                                                                                                                                            cancer; human.
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                   02-APR-2003
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                                                                                                   AAE33410;
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Best Local S
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                             AAE33410
RESULT
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Gaps

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Score 198; DB 8; Length 60; Pred. No. 1.2e-14; 0; Mismatches 5; Indels

31.94;

Best Local Similarity 88.0 Matches 39; Conservative

Query Match

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Zsig33; gastric motility, gastrointestinal inflammation, reflux disease, nutrient absorption regulation; obesity; metabolic disorder.
                                                                                                                                                                                                                                                 Human polypeptide having homology to motilin, zsig33 - useful e.g. to treat gastrointestinal motility disorders, obesity etc. and to identify antagonists to treat gastrointestinal hypermotility.
                                                                                  24. .117 ______/note= "mature protein"
                                                                   1. .23
/note= "signal peptide"
                                                                                                                                                                                                                                                                                    Claim 13; Page 55-56; 69pp; English.
                                                          Location/Qualifiers
                                                                                                                                                            97US-0041102P
                                                                                                                                              98WO-US005620
Protein designated zsig33.
                                                                                                                                                                                       (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                         Deisher TA;
                                                                                                                                                                                                                          WPI; 1999-070071/06.
                                                                                                                                                                                                                                  N-PSDB; AAX04550
                                                                                                                                                                                                        Sheppard PO,
                                                                                                                                                              24-MAR-1997;
24-MAR-1997;
                                          Homo sapiens
                                                                                                                                              23-MAR-1998;
                                                                                                             WO9842840-A1
                                                                                                                             01-OCT-1998
                                                                  Peptide
                                                                                    Protein
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The present sequence represents a protein designated Zsig33. The nucleic acids are strongly expressed in stomach tissue. The polypeptide (or acids are strongly expressed in stomach tissue. The polypeptide (or allelic variants/orthologs) can be used to stimulate gastric motility, measured as increased transit time or gastric emptying of an ingested substance in mammals. The products are used to treat disorders associated with gastrointestinal cell contractility, secretion of digestive enzymes, gastrointestinal inflammation, reflux disease and nutrient enzymes, gastrointestinal inflammation, reflux disease and nutrient concording protein motilin belongs has been associated with neurological concording functions. They may therefore be used e.g. to regulate satiety or treat obesity and other metabolic disorders where neurological feedback modulates nutritional absorption. They are useful to identify zsig33 agonists, antagonists and ligands and to produce antibodies

Sequence 117 AA;

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Gaps
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31.9%; Score 198; DB 2; Length 117;
88.6%; Pred. No. 2.8e-14;
tive 0; Mismatches 5; Indels
                                                                            1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP 44
                                                                                                   1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 44
                                        39; Conservative
                      Best Local Similarity
      Query Match
                                        Matches
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AAY87236 standard; protein; 117 AA RESULT 5

AAY87236;

11-MAY-2000 (first entry)

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Gapa

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1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP 44

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Length 117; 5; Indels

31.9%; Score 198; DB 3; 88.6%; Pred. No. 2.8e-14; 0; Mismatches

Conservative

Best Local Similarity Matches 39; Conserv

Query Match

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Sequence 117 AA;

Human signal peptide containing protein HSPP-13 SEQ ID NO:13

Human; signal peptide-containing protein; HSPP; diagnosis; cancer;

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                  antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic; antiasthmatic; gene therapy; cell proliferation; neurological disorder; reproductive disorder; developmental disorder; arteriosclerosis; cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia; asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia; Parkinson's disease; Huntington's diseases; ovulatory defect;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gorgone GA, Corley NC, Guegler KJ, Baughn MR; foung J, Yue H, Patterson C, Reddy R, Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to AAZ98242 encode AAY87224 to AAY87357 which represent the
inflammation; cardiovascular disease; anticancer; anti-inflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 168-169; 327pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            99WO-US014484.
                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0090762P.
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98US-0112129P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Au-Young J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-160673/14.
                                                                                                                                                                                       muscular dystrophy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAZ98121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (INCY-) INCYTE
                                                                                                                                                                                                                                                                                           VO200000610-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Akerblom IE,
                                                                                                                                                                                                                                           Ното варіеня
                                                                                                                                                                                                                                                                                                                                                                                            25-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1998;
                                                                                                                                                                                                                                                                                                                                               06-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bandman O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lal P,
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gastric contractility; nutrient uptake; digestive; pancreatic; human; insulin-like growth factor-1; growth hormone; bone; gastrointestinal; glucose; osteopathic; anorectic; vulnerary; immunomodulator; GHS-R;

G-protein coupled receptor

Homo sapiens

Key Peptide

hormone; enzyme; neural development;

transduction;

zsig33; signal

(first entry)

23-JUL-2001 AAB62649;

Human zsig33 polypeptide.

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The present sequence is that of zsig33, a secreted protein with homology to motilin (see AAB20102). Zsig33 is expressed at high levels in the secondary and at lower levels in the small intestine and pancreas. A novel peptide fragment of zsig33, termed SGIP (see AAB20100), is claimed. SGIP is a ligand for growth hormone secretagogue receptor, and is therefore useful for modulating secretion of growth hormone and insulin like growth factor 1. SGIP, and variant SGIP peptides, are used in claimed methods for stimulating contractability in duodenum or jejunum tissue, modulating pancreatic secretion of hormones and digestive enzymes, inducing growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel variants of SGIP peptides for modulating contractility in duodenum or jejunum tissue, pancreatic secretion of hormones and digestive enzymes, inducing growth hormone secretion or modulating gastric
                                                                                                                   SGIP; zsig33; anorectic; antidiabetic; somatotropin; somatomedin-C; nutritional absorption modulator; growth hormone secretagogue; therapy;
                                                                                                                                                                                                                                                                                              /label= SGIP_peptide
/note= "this_peptide is claimed in Claim 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hormone secretion, and modulating gastric emptying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bishop PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Deisher TA,
                                                                                                                                                                                                                                                    24. .117
/label= Mature protein
                                                                                                                                                                                                                           l. .23
/label= Signal_peptide
                                                                                                                                                                                                           location/Qualifiers
AAB20101 standard; protein; 117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; 54; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-2000; 2000WO-US018306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sheppard PO, Jaspers SR,
                                                         23-APR-2001 (first entry
                                                                                                                                                                                                                                                                                 24. .34
/label= :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ZYMO ) ZYMOGENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-123010/13.
N-PSDB; AAF30033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 117 AA;
                                                                                        2sig33 protein.
                                                                                                                                                                                                                                                                                                                                                WO200100830-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUN-1999;
                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                             04-JAN-2001
                            AAB20101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      emptying
                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                        Protein
                                                                                                                                                   human.
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Forming reversible peptide receptor complex for purifying cell and peptides, stimulating signal transduction and modulating hormone secretion, involves contacting a receptor with zsig33 polypeptide.

Claim 1; Page 93-94; 111pp; English

Bishop PD;

Deisher TA,

Sheppard PO, Jaspers SR,

WPI; 2001-355879/37. N-PSDB; AAF83678.

(ZYMO) ZYMOGENETICS INC

22-NOV-2000; 2000WO-US032074.

WO200138355-A2

99US-0166765P.

22-NOV-1999;

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The invention relates to a method of forming a reversible peptide-
creceptor complex that involves providing an immobilized receptor, and
contacting the receptor with a zsig33 peptide (Comprising residues 24-37
of AABS6649), where the receptor binds to the zsig33 peptide. The method
creamsduction in a cell expressing a receptor. It is also useful for
cransduction in a cell expressing a receptor. It is also useful for
contactility, nutrient uptake, secretion of digestive and
contactility, nutrient uptake, secretion of digestive and
contaction of non-zsig33 proteins. It is useful for modulating growth
contaction of non-zsig33 proteins. It is useful for modulating growth
contaction of non-zsig33 proteins. It is useful for modulating growth
contaction of non-zsig33 proteins. It is useful for modulating growth
contaction of non-zsig33 proteins. It is useful for modulating growth
cremodeling, low ostcoblast levels, cartilage repair and remodeling,
cremodeling, low ostcoblast levels, cartilage repair and remodeling,
captetal dysplasia, immune suppression, obesity, growth retardation,
contaction, quantom dealing and ovulation induction, treating a mammal having
a metabolic disorder requiring neurological feedback, such as satiety
contaction, protein and metabolism and neuropathy-sasociated
contaction, disorder and evelabolism and neuropathy-sasociated
contactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gastrointestinal disorders, and stimulating glucose-induced insulin release in a mammal. The present sequence represents the human zsig33 polypeptide, a peptide ligand for the G-protein coupled receptor, GHS-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHORVQVRPPHKAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.9%; Score 198; DB 4;
88.6%; Pred. No. 2.8e-14;
tive 0; Mismatches 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity 88.6
39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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Gaps

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31.9%; Score 198; DB 4; Length 117; 88.6%; Pred. No. 2.8e-14; tive 0; Mismatches 5; Indels

Local Similarity 88.6 nes 39; Conservative

Best Loc Matches

Query Match

1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP 44

AAB62649 standard; protein; 117 AA

AAB62649 ID AAB6 XX RESULT 7

1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP

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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polymucleotides are useful immunosuppressant and cytostatic activity. The polymucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as and central nervous injuries, peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, and such as a lateral sclerosis, and Shy-Drager Sydrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, hemotactic/chemokinetic activity, hemotactic/chemokinetic activity, hemotactic/chemokinetic activity, nancer diagnosis and thrombolytic activity, cancer diagnosis and inflammation, leukaemias and assays for receptor activity, arthritis and inflammation, leukaemias and constant diagnosis constant did not form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.
                                                                                                                                                             peripheral nervous system; neuropathy; central nervous system; CNS; Alzhaimer's; Parkinson's disease; handrington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-brager Syndrome; chemotactic; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ma Y,
Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; SEQ ID NO 2035; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu C, Aeundi V, Chen R,
Wang Z, Wehrman T, Xu C,
Goodrich R, Drmanac RT;
                                                                                                                                               immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        part of the printed specification
                                                                                                            Human polypeptide SEQ ID NO 2035.
             AAM38890 standard; protein; 117
                                                                                                                                                                                                                                                                                                                                                                                               99US-00471275.
2000US-00488725.
2000US-00598042.
2000US-00598042.
2000US-00623450.
2000US-00653450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-OCT-2000; 2000US-00693036.
29-NOV-2000; 2000US-00727344.
                                                                                                                                                                                                                                                                                                                                                                26-DEC-2000; 2000WO-US034263
                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-442253/47.
N-PSDB; AAIS8046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 117 AA;
                                                                                                                                                                                                                                                                                                WO200153312-A1
                                                                                                                                                                                                                                                                                                                                                                                                                  21-JAN-2000;
25-APR-2000;
20-JUN-2000;
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14-SEP-2000;
19-OCT-2000;
                                                                               22-OCT-2001
                                                                                                                                                                                                                                                                                                                                 26-JUL-2001
                                                                                                                                                                                                                                  leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang J,
Zhou P,
                                              AAM38890;
                                                                                                                                                                                                                                                                 Homo
AAM38890
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The invention relates to a movel peptide compound or its salt which induces the secretion of growth hormone and/or elevates calcium ion concentration in cells. The peptides are ghrelin homologues and are characterised in that at least one amino acid has been substituted by a modified amino acid and/or a non-amino acid compound. The invention also encompasses the unmodified peptides; the DNA encoding the peptides; vectors and host cells comprising such DNA, a method of producing the peptides comprising recombinant production, optionally followed by chemical modification; an antibody specific for a peptide of the invention and an assay and kit for detecting the peptides. The peptides of the invention are useful for treating and/or diagnosing diseases caused by a deficiency in growth hormone expression or activity. In particular, they are useful for promoting infant growth due to growth hormone deficiency. The compounds of the invention are safe with no accompanying side effects. The present sequence represents a ghrelin-type growth hormone secretagogue (GHS) precursor protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New peptide compounds which induce growth hormone secretion and elevate cell calcium concentrations, useful in treatment and diagnosis of infant growth disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                       Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein; calcium concentration elevation; infant growth disorder; growth hormone deficiency.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31.9%; Score 198; DB 4; Length 11
88.6%; Pred. No. 2.8e-14;
ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 182; 210pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hosoda H,
             AAB60511 standard; protein; 117
                                                                                                                                                                                                                                                                                                                                                                                23-JUL-1999; 99JP-00210002.
29-NOV-1999; 99JP-00338841.
26-APR-2000; 2000JP-00126623.
                                                                                                                        Human ghrelin preproprotein,
                                                                                                                                                                                                                                                                                                                                               24-JUL-2000; 2000WO-JP004907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query March
Best Local Similarity 88.6
Matches 39, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kangawa K, Kojima M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-159704/16.
N-PSDB; AAF59645.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KANG/) KANGAWA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 117 AA;
                                                                                                                                                                                                                                                                        WO200107475-A1
                                                                                                                                                                                                                                        Homo sapiens
                                                                                    24-APR-2001
                                                                                                                                                                                                                                                                                                             01-FEB-2001.
                                                 AAB60511;
AAB6051.
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Wang D; Zhao QA;

Ren F, Wa

Qian XB, Yang Y,

Query Match
31.9%; Score 198; DB 4; Length 117;
Best Local Similarity 88.6%; Pred. No. 2.8e-14;
Matches 39; Conservative 0; Mismatches 5; Indels

ABB78319 standard; protein; 117 AA.

RESULT 10 ABB78319 ID ABB7

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Gaps

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Key

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Disclosure; Page 27; 34pp; English
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                                                                                                                                                       10-MAY-2001; 2001US-00853253
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                                                                                                                                                                                                                                                                                                    Jaspers SR, Sheppard PO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity 88.6
39; Conservative
                                                                                                                                                                                                                   JASPERS S R.
SHEPPARD P O.
DEISHER T A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human zsig33 protein.
                                                                                                                                                                                                                                                                                                                                WPI; 2002-443750/47
                                                                                                                                                                                                                                                                     BISH/) BISHOP P D.
                                                                                                                                                                                                                                                                                                                                                N-PSDB, AAD38238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 117 AA;
                                                                                           JS2002055156-A1.
                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAR-2002
                                                                                                                           39-MAY-2002
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Best Local S
                                                                                                                                                                                                                       JASP/)
                                                                                                                                                                                                                                     SHEP/)
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AAE15883
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Matches
%XCCCCCCCCCCCCCXXXX4445X3X35X53X5X6X6X6X6X4X6X8X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents human zsig33. The specification describes a short gastrointestinal peptide (SGIP), which is derived from zsig33.

SGIP has homology to motilin. The SGIP peptide may be used in the prevention, disgnosts and treatment of diseases associated with inappropriate SGIP expression. For example, SGIP may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient, s genome that affect the activity of SGIP by expression in active proteins or to supplement the patients own production of SGIP. SGIP may also be used as an antigen in the production of antibodies against SGIP and in assays to identify modulators of SGIP in antibodies may also be used to regulate expression and activity. The anti-SGIP antibodies, agonists and anti-SGIP antibodies, agonists may also be used to regulate expression and activity. The anti-SGIP antibodies against for detecting the presence of SGIP in samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Short Gastrointestinal Peptide, which has homology to motilin, preventing, diagnosing and treating gastrointestinal disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP
                                                                                                            Short gastrointestinal peptide; SGIP; zsig33; motilin.
                                                                                                                                                                                                                                                                                                                                                                                                                                Bishop PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.9%; Score 198; DB 5;
88.6%; Pred. No. 2.8e-14;
iive 0; Mismatches 5;
                                                                                                                                                                                                        /note= "signal peptide"
                                                                                                                                                                                                                                         /note≈ "mature protein'
                                                                                                                                                                                                                                                                                                                                                                                                                                Deigher TA,
                                                                                Amino acid sequence of a human zsig33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Col 39-40; 23pp; English.
                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                  99US-0141592P
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                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similaric,
nes 39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   (ZYMO ) ZYMOGENETICS INC.
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N-PSDB; ABV72214.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 117 AA;
                                                                                                                                                                                                                                                                                                                                                                    30-JUN-1999;
                                                                                                                                              Homo sapiens
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                                                 05-DEC-2002
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                  ABB78319
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                                                                                                                                                                                                                           Protein
                                                                                                                                                                                           Peptide
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New

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The invention relates to zsig33-like peptides and their corresponding nucleic acids and methods for modulating gastric contractility, nutrient uptake, growth hormones, secretion of digestive enzymes and hormones. The sequences of the invention are used in the prevention, diagnosis and treatment of diseases associated with inappropriate 2SIG33 expression.

The nucleic acids of the invention and their complements are used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The ZSIG33 peptides are used as antigens in the production of antibodies against ZSIG33 peptides are used as antibodies and antagonists are used to down regulate expression and activity. The anti-ZSIG33 antibodies are also used as diagnostic agents for detecting the presence of ZSIG31 in samples (e.g. by enzyme linked immunosorbent assay (BLISA)). The peptides and nucleic acids of the invention are used to modulate gastric contractility, nutrient uptake, growth hormones, the escretion of digestive enzymes and hormones in the pancreas. Zaig33-like DNA is used in gene therapy and zsig33-like peptide is used in protein therapy. The present sequence is human zsig33 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZSIG33-Like peptides and polynucleotides, useful for modulating gastric contractility, nutrient uptake, growth hormones and/or secretion of digestive/pancreatic enzymes and hormones.
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Human; zsig33-like peptide; gastric contractility; nutrient uptake;
growth hormone; digestive enzyme; restorative therapy; gene therapy;
protein therapy; gastrointestinal; endocrine; anabolic.
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Matches

RESULT 11

AAE23838

stomach; liver;

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Homo sapiens
          22-NOV-2001
                      peptides.
     Peptide
       Protein
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Human; PRO; cytostatic; tumour; cancer; breast; lung;
horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
antibody-dependent enzyme mediated prodrug therapy.
                                                       ABUS8046 standard; protein; 117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0049787P.
97US-00622069.
97US-0065111P.
97US-0065311P.
98US-0078910P.
98US-0078910P.
98US-0083322P.
98US-008332P.
98US-008322P.
98US-008759P.
98US-0087607P.
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9805-0088028P-
9805-0088039P-
9805-0088033P-
9805-0088126P-
9805-0088127P-
9805-0088127P-
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9805-008855P
9805-0088734P
9805-0088742P
9805-0088742P
9805-0088810P
9805-0088824P
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9805-0088876P-
9805-0089105P-
9805-0089512P-
9805-0089514P-
9805-0089538P-
9805-0089538P-
9805-0089538P-
9805-0089598P-
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98US-0089801P.
98US-0089907P.
98US-0089908P.
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                                                                                                                                   (first entry)
                                                                                                                                                                       Human PRO polypeptide #78.
                                                                                                                                                                                                                                                                                                                            US2003027163-A1.
                                                                                                                                                                                                                                                                                        Homo sapiens.
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04-JUN-1998;
04-JUN-1998;
04-JUN-1998;
04-JUN-1998;
04-JUN-1998;
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                                                                                                                                 14-APR-2003
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07-MAY-1998;
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17-JUN-1998
                                                                                             ABU58046;
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                     RESULT 13
ABU58046
                                                                             The invention relates to zaigl3-like pepticus (25312P) including zaigl3-pepticus to zaigl3-beta, zaigl3-gamma, zaigl3-delta and zaigl3-epailon peptides and nucleic acid molecules encoding such zaigl3-like peptides.

25312P peptides activate the immune system in boosting immunity to infectious diseases, treating immunocompromised patients such as human immunodeficiency virus (HIV) patients, in improving vaccines and in mercitous content on are used to identify and isolate receptors involved in the invention are used to identify and isolate receptors involved in growth regulation in the liver, blood vessel formation and other contentions of tumour cells, as additives to anti-hypoglycaemic processes. They are useful for evaluating functions of hypothalmus-pituitary-adrenal axis, to modulate growth and/or differentiation of tumour cells, as additives to anti-hypoglycaemic preparations containing glucose and as adsorption enhancers for oral natural release. They are also useful as research reagents for the catuge which require fast nutrient action and to stimulate glucose-induced insulin release. They are also useful as research reagents for the expansion, differentiation, growth factor and hormone secretion and/or cell-cell interactions of tissues associated with gastrointestinal system, brain and central nervous aystem. These molecules are useful for treating dysfunction associated with contractility, secretion of digestive enzymes, hormone and acids, secretion of hormones in the pancreas and/or brain, gastrointestinal contractility, secretion of digestive enzymes, inflammation and regulation contractility, recruitment of digestive enzymes, inflammation and regulation contractility, secretion of sequences of the invention are useful in gene contractility, and acides associated with inservation and regulation of nutrient absorbers associated with inservation and regulation of nutrient absorbers associated with inservation and regulation of nutrient absorption of houring and acids, secretion of december of the pancr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polypeptides, useful for modulating gastric contractility, nutrient uptake, pancreatic secretion of hormones, digestive enzymes and treating gastrointestinal and growth related diseases, comprises zsig33-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention relates to zsig33-like peptides (ZS33LP) including zsig33-
infection; human immunodeficiency virus; vaccine; antihypoglycaemic; adsorption enhancer; gastrointestinal disease; growth related disease; inflammation; gene therapy; growth regulation; blood vessel formation; HIV; zsig33 protein.
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/note= "Human mature zaig33 protein"
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/label= Signal_peptide
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17-AUG-1999; 99WC-01821290.
18-SEP-1999; 99WC-01821547.
08-OCT-1999; 99WC-01828313.
01-DEC-1999; 99WC-01828313.
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01-DEC-1999; 99WC-018028313.
02-DAN-2000; 99WC-018028011.
05-JAN-2000; 2000WC-0180011.
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24-FEB-2000; 2000WC-018011.
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25-MAX-2000; 2000WC-018011.
26-JUL-2000; 2000WC-018011.
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ABU59124 standard; protein; 117

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Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing; cardiac insufficiency disorder; cancer; tumour; immune response; adrenal cortical capillary endothelial growth, c-fos induction; vascular endothelial growth factor inhibition; VEGF inhibition; endothelial growth inhibitor; T-lymphocytes stimulation; retinal neurons cell survival; rod photoreceptor cell survival; retinal disorder; retinitis pigmentosum; kidney disorder; mammalian kidney mesangial cell proliferation; Berger disease; dermatitis; herpetiformis; Crohn's disease; chondrocyte proliferation; chondrocyte redifferentiation; sports injury; arthritis.
                   human secreted or transmembrane protein PRO1066.
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WPI; 2003-247083/24. N-PSDB; ABX80294.

Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes are therapeutically useful for enhancing immune response and in cancer treatments.

Claim 12; Fig 186; 648pp; English.

The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in linking a bloactive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus useful for trearing cardiac insufficiency disorders. PRO154 and PRO186 stimulate adrenal cortical capillary endothelial growth, and PRO536, PRO943, PRO828, PRO186 or PRO555, PRO826, PRO819, PRO126, PRO186 or PRO155, prosellar and is thus useful for treating conditions or disorders where anglogenesis would be beneficial, e.g. wound healing and antagonist of this polypeptide are

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9805-0090252P

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    useful for treating cancerous tumours. PROB12 inhibits vascular endothelial growth factor (VEGF) stimulated proliferation of endothelial cells and is thus useful for inhibiting endothelial cell growth in mammals which would be beneficial in inhibiting tumour growth. PROB26, PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of enfoncing entimulated T-lymphocytes and are therapeutically useful for enhancing immune response. PROB26, PRO1058 or PRO1132 enhance survival of retinal neurons cells (PRO1132 is also enhances survival/proliferation of rod photoreceptor cells) and therefore are useful for treating retinal disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO813 and therefore are useful for treating kidney disorders associated with dermatitis, herpetiformis or Crohn's disease. PRO1310, PRO844, PRO1132, PRO1132 and PRO1387 induce the copincation and/or redifferentiation of chondrocyces in culture and are thus useful for treating sports injuries, and arthritis. This is the amino acid sequence of a novel human PRO protein
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PR 04-AUG-1998, 98US-0095282P.
PR 04-AUG-1998, 98US-00953101P.
PR 04-AUG-1998, 98US-00953102P.
PR 04-AUG-1998, 98US-00953102P.
PR 10-AUG-1998, 98US-0095312P.
PR 10-AUG-1998, 98US-0095312P.
PR 11-AUG-1998, 98US-0095312P.
PR 11-AUG-1998, 98US-0095325P.
PR 11-AUG-1998, 98US-0095325P.
PR 11-AUG-1998, 98US-0095325P.
PR 11-AUG-1998, 98US-0095727P.
PR 12-AUG-1998, 98US-0095727P.
PR 25-AUG-1998, 98US-0095727P.
PR 26-AUG-1998, 98US-0095727P.
PR 26-AUG-1998, 98US-0095727P.
PR 26-AUG-1998, 98US-0097737P.
PR 26-AUG-1999, 98US-0097737P.
PR 26-AUG-1999, 98US-0103797P.
PR 26-AUG-1999, 98US-0103797P.
PR 26-AUG-1999, 98US-0103797P.
PR 26-AUG-1999, 98US-011329F.
PR 26-AUG-1999, 98U
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

December 21, 2005, 13:26:47; Search time 38 Seconds (without alignments) 296.246 Million cell updates/sec

US-10-659-782B-32

620 1 MPSPGTVCSLLLLGMLWLDL......PPSSRERSRRSHQPSCSPEL 117 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:* Database

1: Pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	ghrelin precursor	ghrelin precursor	regulator of nucle	hypothetical prote	anti-mullerian hor	virulence-associat	hypothetical prote	hypothetical prote	thyrotropin recept	lyase - Pseudomona	interleukin-1beta	unknown protein Fl	probable membrane	hypothetical prote	retrotransposon li	hypothetical prote	thyrotropin recept	l pr	sensor protein Bas	sensor protein for	•~	hypothetical 51.8K	probable MYB famil	interleukin-1beta	interleukin-1beta	conserved hypothet		_	bifunctional cycla
ID	A59316	B59316	AG0449	T34274	JC4335	E64211	H83043	T22943	I48882	877905	A56084	H96792	562048	T32425	B85188	E71436	A35956	T51876	F91265	C86106	JX0285	C39926	G84707	C56084	B56084	A75560	JH0634	T28897	S25080
DB	-	٦	~	~	~	٦	~	~	N	~	~	~	~	~	~	~	~	N	N	N	N	N	~	~	~	~	~	~	7
% Query Match Length	117	117	136	2018	573	725	555	999	764	309	383	302	1487	196		~		187		363	363		519			749	428	1001	304
* Query Match	31.9	25.5	12.6	11.9	11.8	11.8	11.7	11.6	11.5	11.4	11.4	11.1	11.1	11.0	11.0	11.0	10.9	10.8	10.8	10.8	10.8	10.8	10.8	10.7	10.7	10.7	10.6	10.6	10.6
Score	198	158	78	73.5	73	73	72.5	72	71.5	70.5	70.5	69	69	68	68	68	67.5	67	67	67	67	67	67	99	66.5	66.5	99	99	65.5
Result No.	-	8	e	4	ۍ ک	y	7	6 0	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

A,Accession: B59316
A,Status: not compared with conceptual translation
A,Rolecule type: mRNA; protein
A,Rolecule type: mRNA; protein
A,Rosidues: 1-117 <KOJ>
A,Rosidues: 1-17 <KOJ>
A,Experimental sources: UNIPROT:090YH7; UNIPARC:UPI000012B411; GB:AB029433; NID:g6691569; PII
A,Experimental source: strain SD; tissue stomach endocrine cells

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hypothetical prote conserved hypothet hypothetical prote	regulatory protein mitosis initiation hypothetical prote	ABC transporter, A serine proteinase probable transmemb	hypothetical prote fission yeast Skbl mitosis initiation	sensory transducti titin - rabbit (fr ribosomal protein	hypothetical prote
T33503 B64187 S16506	S32932 A38436 T19507	G75548 S45493 T36589	T27400 T03842 T13648	S77175 S20901 a57296	T19409
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307 1027 381	4 1 1 2 1 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1	354 467 502	540 637 695	749 6805 221	746
10.6	. 4. 4. E.	10.3	1001	10.3	10.2
65.5 65 7	64.5 64.5 64.5	4 4 4 4	0 0 0 4 4 4	64	63.5
30	3 W W W W W W W W W	36 37 38	9 4 4 9 0 0 1	4 4 4 2 6 4	4.5

AL IGNMENTS

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A; Molecule type: mRNA
A; Residues: 1-17 * KGO>
A; Cross-references: UNIPROT: 09UBU3; UNIPARC: UPI00000362D3; GB:AB029434; NID:g6691571; PII
A; Experimental source: tissue stomach endocrine cells
A; Experimental source: tissue stomach endocrine cells
A; Note: submitted to GenBank, June 1999
C; Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (growth C; Superfamily: motilin
C; Keywords: hormone; lipoprotein; stomach
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-51/Product: ghrelin #status predicted <MAT>
F;24-13/Product: ghrelin #status predicted <MAT>
F;22-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;26/Binding site: octanoate (Ser) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ghrelin precursor - rat

N.Alternate names: preproghtelin

CiSpecies: Rattus norvegicus (Norway rat)

CiDate: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 09-Jul-2004

CiDate: 16-Jun-1000 #sequence_revision 16-Jun-2000 #text_change 09-Jul-2004

CiDate: 16-Jun-1000 #sequence_revision 16-Jun-2000 #text_change 09-Jul-2004

CiAccession: B59316

Rikolina, M.; Hosoda, H.; Rangawa, K.

Nature 402, 656-660, 1999

A;Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.

A;Reference number: A59316; MUID:20067959; PMID:10604470
                                                                                                                                    C;Accession: A55316
R;Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.
R;Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.
Nature 402, 656-660, 1999
A;Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.
A;Reference number: A59316; MUID:2006/959; PMID:10604470
A;Accession: A59316
A;Status: not compared with conceptual translation
                                                                          C;Species: Homo sapiens (man)
C;Spacies: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 31.9%; Score 198; DB 1; Length 11 Best Local Similarity 88.6%; Pred. No. 1.7e-13; Matches 39; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHORVQVRPPHKAP 44
                                         N; Alternate names: preproghrelin
ghrelin precursor - human
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B59316
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95

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Virulence-associated protein vacB homolog - Mycoplasma genitalium C;Species: Mycoplasma genitalium C;Species: Mycoplasma genitalium C;Species: Mycoplasma genitalium C;Species: Mycoplasma genitalium C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C;Date: 10-Sep-1999 #sequence_revision 10-; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.N., C.A.; Venter, J.C. Science C, 37-403, 1995 Science C, 37-403, 1995 A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Title: The minimal gene complement of Mycoplasma genitalium.
                    A,Introns: 16/2; 52/3; 87/2; 116/2; 138/2; 203/1; 265/3; 317/2; 337/3; 378/1; 428/1; 482/
7/3; 1491/3; 1560/2; 1632/2; 1753/3; 1830/2; 1862/2; 1927/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: JC4335
R;Visser, J.A.; McLuskey, A.; van Beers, T.; Weghuis, D.O.; van Kessel, A.G.; Grootegoed, Biochem. Biophys. Res. Commun. 215, 1029-1036, 1995
A;Title: Structure and chromosomal localization of the human anti-muellerian hormone type A;Reference number: JC4335; MUID:96028015; PMID:7488027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Cross-references: UNIPROT:Q16671; UNIPARC:UP1000016A54B; GB:X91156; NID:g1107671; PIDN:
C,Comment: This is a receptor for anti-mullerian hormone (see PIR:WFHUM). It plays a crit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GDB:696210; OMIN:600956
A;Map position: 12q13-12q13
A;Introns: 16/3; 17/3; 14/13; 16/7; 284/2; 322/3; 380/2; 429/3; 475/2
A;Introns: 16/3; 77/3; 14/13; 16/7; 1284/2; 322/3; 380/2; 429/3; 475/2
C;Keywords: ATP; hormone receptor; transmembrane protein
F;1-16/Domain: signal sequence #status predicted <SIG>F;1-573/Product: anti-muellerian hormone type II receptor #status predicted <MAT>F;17-141/Domain: extracellular hormone binding #status predicted <ELB>F;142-167/Domain: transmembrane #status predicted <TWM>F;12-167/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anti-mullerian hormone type II receptor precursor - human
C;Species: Homo sapiens (man)
C;Date: 06-Dec-1995 #sequence_revision 08-Feb-1996 #text_change 05-Oct-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188 DSGRDWSVELQELP---ELC------FSQVIREGGHAVWAGQLQGKLVAIKAF
                                                                                                                                                                                                                                                                                                               652 RIPHFIDEIKLSLP-----CDLNDGHHLLFTVYHISCKEGDSSSTESPIGYTW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45 H-----VVPALPLSNQLCDLEQQRHLWASVFSQSTKDSGSDLTVSGRTWGLRVLNRLF
                                                                                                                                                                                                                                                      38 RPPHKAPHVVPALPLSNQLCDLEQQRHLWASVFSQSTKDSGSDLTVS--GRTWGLRVLNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 SPGTVCS------LLLLGMLWLDLAMAGS---SFLSPEHQRVQVRP-PHKAP
                                                                                                                                                                                       Gaps
                                                                                                                                                                                    31; Indels 17;
                                                                                                          Query Match
11.9%; Score 73.5; DB 2; Length 2018;
Best Local Similarity 31.2%; Pred. No. 37;
Matches 25; Conservative 7; Mismatches 31; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.8%; Score 73; DB 2; Length 573; 27.4%; Pred. No. 10; tive 15; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                     96 LFP--PSSRERSRRSHQPSC 113
                                                                                                                                                                                                                                                                                                                                                                                                                                              700 -LPLYRNGKLRSGNFHLPVC 718
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A; Residues: 1-573 <VIS>
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A; Map position: X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: GDB: AMHR2
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Arither Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q8ZAU1, UNIPARC:UPI0000DCABC; GB:AL590842; PIDN:CAC93163.1;
C;Genetics:
A;Gene: rnk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-2018 <NHA>
A;Cross-references: UNIPROT: Q20487; UNIPARC: UPI0000081BE1; EMBL: U41543; PIDN: AAB37023.1;
A;Experimental source: strain Bristol N2; clone F46H5
                              C.Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (growt
C,Superfamily: motilin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regulator of nucleoside diphosphate kinase rnk [imported] - Yersinia pestis (strain CO94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>ښ</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAPHVVPALPLSNQLCDLE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMAGS---SPLSPEHORVQVRPPHKAPHVVPALPLSNQLCDL-EQQRHLWASVFSQSTKD 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MVSSATICSLILLSMLWMDMAMAGSSFLSPEHQKAQQRKESKKP-----PAKLQPRALE 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein F46H5.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26; Gaps
                                                                                      SGSDLTV------SGRTWGLRVLNRLFPPSS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNEQLSVMAPLGAALLGLHVNDEISWKLPGGDETRITVLELLYQPES 130
                                                                                                                                                                                                                                                                                        Query Match 25.5%; Score 158; DB 1; Length 117; Best Local Similarity 40.0%; Pred. No. 2.5e-09; Matches 42; Conservative 7; Mismatches 34; Indels 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GWLHPEDRGQAEEAEEELEIRFNAPFDVGIKLSGAQYQQHGRALG 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39; Indels
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A;Reference number: Z21498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
0.64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, November 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
12.6%; Score 78; DB 2
Best Local Similarity 26.2%; Pred. No. 0.64;
Matches 28; Conservative 14; Mismatches
      submitted to GenBank, June 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Molecule type: DNA
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A;Gene: CESP:F46H5.4
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C,Accession: 148882
R;Stein, S.A.; Oates, E.L.; Hall, C.R.; Grumbles, R.M.; Fernandez, L.M.; Taylor, N.A.; P. Mol. Endocrinol. 8, 129-138, 1994
A;Title: Identification of a point mutation in the thyrotropin receptor of the hyt/hyt h;
A;Reference number: A54271; MUID:94224232; PMID:8170469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A Status: preliminary
A Molecule type: manA
A Residues: 1.764 RESA
A, Cross-references: UNIPROT: P47750; UNIPARC: UPI0000003F87; EMBL: U02602; NID: 9575923; PID)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat hc C; Superfamily: ductine-coupled receptor; transmembrane protein  
F;53-76/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;77-101/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;77-101/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;127-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;152-176/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;152-176/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;179-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;179-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;170-226/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
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C;Species: Pseudomonas pseudomallei
C;Species: 21-Apr-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C;Accession: 877905; S36445; S3644 ferrera-Estrella, L.; Bailey, A.M.
R;Penaloza-Vazquez, A.; Mena, G.L.; Herrera-Estrella, L.; Bailey, A.M.
Appl. Environ. Microbiol. 61, 538-543, 1995
A;Trle: Cloning and sequencing of the genes involved in glyphosphate utilization by Pseu A;Reference number: S77905; MUID:96031567; PMID:7574593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues 1.-30 eRBN.
A;Cross-references: UNIRROT:Q52502; UNIPARC:UPI00000B6398; EMBL:X74325; NID:g439726; PIDN
A;Experimental source: strain 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 PGTVCSLLLLGMLWLDLAMAGSSFLSPE---HQRVQVRPPHKAPHVVPALPLSNQLCDLE 60
                                                                                                                                                                                                                                                                                                                                                                                                       81 LTVSGRTWGLRVLNR------LFPPSS-----RERSR----RSHQPSCSPEL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N.Alternate names: thyroid-stimulating hormone receptor; TSH receptor
C;Species: Mus musculus (house mouse)
C;Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                        3 PGSL--LLLVLLLALSRSLRGKECASPPCECHQEDDFRVTCKELHRIPSLPPSTQTLKLI
                                                                                                                                                                                                                                                             33 QRVQVRPPHKAPHVVPALPLSNQLCDLEQQR-HLWASVFSQSTKDSGSD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
11.5%; Score 71.5; DB 2; Length 764;
Best Local Similarity 28.8%; Pred. No. 21;
Matches 32; Conservative 16; Mismatches 50; Indels 13; Gaps
                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 QQ--RHLWASVFSQSTKDSGSDLTVSGRTWGLRVLNRLFPPSSRERSRRSH 109
                                                                                                                                                                                                  34;
                                                                                                                           Query Match
11.6%; Score 72; DB 2; Length 666;
Best Local Similarity 26.9%; Pred. No. 16;
Matches 32; Conservative 11; Mismatches 42; Indels
A;Gene: CESP:F58G11.3
A;Map position: 5
A;Introns: 42/2; 82/2; 153/3; 274/3; 380/1; 569/3; 613/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thyrotropin receptor precursor - mouse
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S77905
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C;Accession: H33043
C;Accession: H33043
G;Stover. C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-555 <STO>
A;Cross-references: UNIPROT:Q9HUX8; UNIPARC:UPI0000C5E23; GB:AE004895; GB:AE004091; NID
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:P90898; UNIPARC:UPI000007850D; EMBL:Z81094; PIDN:CAB03154.1; A;Experimental source: clone F58G11
                                                                                           A;Cross-references: UNIPROT:P47350; UNIPARC:UPI00001344B5; GB:U39690; GB:L43967; NID:gld
A;Experimental source: strain G-37
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 LDLAMAGSSFLSPEHORVQVRPPHKAP-----HVVPALP--LSNQLCDLEQQRHLWAS 68
                                   Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein PA4822 [imported] - Pseudomonas aeruginosa (strain PAOI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein F58G11.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Pseudomonas aeruginosa
Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                              20;
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                                                                                                                                                                                                                                                                                                                                               DB 1; Length 725;
                                                                                                                                                                                                                                                                                                                                           11.8%; Score 73; DB 1; Length 725 25.7%; Pred. No. 14; arive 16; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 VFSQSTKDSGSDLTVSGRTWGLRVLNRLFPPSSRERSRRSH 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VFSQSTKDSGSDLTVSGRTWGLRVLNRLFPPSSRERSRR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   460 AFLREDLDAALRLVAR----KKLLQRLEADASRERFRR 493
                                                                                                                                                                                                                                            A;Genetic code: SGC3
C;Superfamily: virulence-associated protein vacB homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species.
C;Date: 15-Oct-1999 #ecg.
C;Date: 15-Oct-19943
C;Accession: T22943
R;Percy, C.
Submitted to the EMBL Data Library, October 1996
A;Reference number: 219640
A;Accession: T22943
A;Accession: T22943
A;Accession: preliminary; translated from GB/EMBL/DDB
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A;Molecule type: DNA
A;Residues: 1-666 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.7%; Score 72.5; Local Similarity 31.3%; Pred. No. 11 les 31; Conservative 9; Mismatchen
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 25.7*
Matches 26; Conservative
                                                                          A; Molecule type: DNA
A; Residues: 1-725 <TIGR>
       A; Accession: E64211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Experimental (C,Genetics:
A,Gene: PA4822
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A; Accession: H96792
A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Crossidues: 1-302 <STO>
A; Crossidues: 1-302 <STO>
A; Crossidues: 1-402 <STO>
A; Crossidues: 1-402 <STO>
A; Crossidues: 1-402 <STO>
A; Crossidues: 1-402 <STO>
A; Crossidues: Fferences: UNIPROT: Q9C9K7; UNIPARC: UPI00000A0BE5; GB: AE005173; NID: g6642668; PII
A; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: S62048
A;Molecule type: DNA
A;Roesdidues: 1-1487 <KLI.>
A;Roesdidues: 1-1487 <KLI.>
A;Cross-references: UNIPROT: P53094; UNIPARC: UPI0000052E6A; EMBL: X91837; NID: g1177627; PII
A;Experimental source: strain FY1679
R;Bruschi, C.V.; Coglievina, M.; Bertani, I.; Klima, R.; Zaccaria, P.; Delneri, D.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64183
A;Accession: S64214
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A.Recidues: 1-1487 <BRU>
A.Cross-references: UNIPARC:UPI000052E6A, EMBL:Z72719; NID:g1322824, PID:e243500, PID:g1
A.Experimental source: strain S288C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 PELHHQLQPQPQLHPLPQPQPQPQQPQQNSDDE-----SDSNKDPGSDPVTSGST 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 PE-HORVOVRPP-HKAPHVVPALPLSNOLCDLEQORHLWASVFSOSTKDSGSDLTVSGRT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable membrane protein YGL197w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein G1307
C;Species: Saccharomyces cerevisiae
C;Species: 10-Apr.1996 #sequence_revision 19-Apr.1996 #text_change 09-Jul-2004
C;Accession: $52048; $64214
R;Xilina, R.; CQalievina, M.; Bertani, I.; Zaccaria, P.; Bruschi, C.V.
A;Reference number: $62045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 SSFLSPEHQRVQVRPPHKAPHKVPPALPL-----SNQLCDLEQ-----QRHLWASVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                           Query Match 11.1%; Score 69; DB 2; Length 302; Best Local Similarity 31.6%; Pred. No. 13; Matches 30; Conservative 6; Mismatches 31; Indels
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F:1034-1050/Domain: transmembrane #status predicted <TM1>
F:1052-1068/Domain: transmembrane #status predicted <TM2>
A; Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 WGLRVLNRLFPPSSRERSR------RSH 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: SGD:S0003165; MIPS:YGL197w
A;Map position: 7L
                                                                                                                                                                                                                                                                           A,Map position: 1
C,Superfamily: AT-hook DNA-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     882 MSTGSNTRRSNTLTDYMHSNKASP 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
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R;Alnemri, E.S.; Fernandes-Alnemri, T.; Litwack, G.
Biol. Chem. 270, 4312-4317, 1995
A;Ittle: Cloning and expression of four novel isoforms of human interleukin-lbeta conver A;Reference number: A56084; MUID:95181414; PMID:7876192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cjacce (W. Chung M.K.) Palm, C.J.; Federapiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung M.K.; Comway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Alaukor, N.F.; Hughes, B.; Huizar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Alaukors, Hunger, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A.; Luros, J.S.; Maiti, R.; Marziali, Ret, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Hitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: UNIPROT:P29466; UNIPARC:UP1000002AB7F; GB:U13697; NID:g717039; PIDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 IPKGAQACQICITYICEEDSYLAGTLGLSAAPQAVQDN------PAMPTSSGSEGNV 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHORVQVRPPHKAPHVVPALPLSN----- 54
                                                                                                                                                                                                                                                                                                                                                  14 PEPGIV-------LSGVHKSRRGRPPQKAAYLARWKYSPIVAADPRA 53
                                                                                                                                                                                                                                                                                                                                                                                                                     54 NQLCDLEQQRHLWASVFSQSTKDSGSDLT-----VSGRTWGL----RVLNRLFP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----GSDLTVSGRTWGL 90
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 05-Oct-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                  2 PSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAPH----
                                                                                                                                       11.4%; Score 70.5; DB 2; Length 3 ilarity 22.0%; Pred. No. 9.6; Conservative 16; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interleukin-lbeta converting enzyme beta isozyme - human
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                                       A;Gene: glpB
C;Superfamily: Pseudomonas pseudomallei lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Gene: IL1BCE
C,Keywords: alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99 PSSRERSRRSHQ 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 RKSLNAAKPSHR 117
                                                                                                                                          Query Match
Best Local Similarity
Matches 29; Conserv
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A,Molecule type: mRNA
A,Residues: 1-383 <ALN>
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              ;Genetics:
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pothetical protein C10E2.3 - Caenorhabditis elegans

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C;Accession: B85188
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin
R;anonymous, 769-777, 1999
A;title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;keference number: A85001; MUID:20083488; PMID:10617198
A;Accession: B85188
                                                                             R;Wohldmann, P.; Sansone, J.
submitted to the EMBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid C10E2.
A;Accession: T32425
A;Accession: T32425
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Roses-references: UNIPROT:017323; UNIPARC:UP10000075F65; EMBL:AF026202; PIDN:AAB71243.
A;Experimental source: strain Bristol N2; clone C10E2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
Kseidues: 1-1474 <STO>
A;Cross-references: UNIPROT:023529; UNIPARC:UPI00000A464B; GB:NC_001268; NID:95302802;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 LDLAMAGSSFLSPEHQRVQV-RPPHKAPHVVPALPLSNQLCDLEQQRHLWASVFSQSTKD 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 LWLDLAMAGSSFL--SPEHQRVQVRPPHKAPHVV---PALPLSNQLCDLEQQRHLWASVF 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            refrotransposon like protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
Species: Caenorhabditis elegans
Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
11.0%; Score 68; DB 2; Length 796;
Best Local Similarity 28.6%; Pred. No. 50;
Matches 28; Conservative 15; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 ------RLKNMIANRSKGESNSQSNLMSNS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 SGSDLTVSGRTWGLRVLNRLFPPSSRERSRRSHQPSCS 114
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C;Superfamily: retrovirus-related polyprotein
                                                        Accession: T32425
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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- permanent accession numbers. The new UniProt record may not contain the previous temporary numbers from the most recent version of UniProt. These sequences have been assigned new Please note that the curators of the UniProt database have purged some temporary accession accession number.
- extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein If you encounter an accession number from an older search run against UniProt (results file Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtm

If you have any questions regarding this information or your results, please contact any STIC searcher

members of the public who may encounter UniProt temporary accession When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or

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GHRL HUMAN STANDARD; PRT; 117 AA.
GHRL 11, Created)
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
13-SEP-2005 (Rel. 48, Last sequence update)
Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide) (M46 protein) [Contains: Ghrelin-27; Ghrelin-28 (Ghrelin)].
Name-GHRL; Synonyms=WTLRP; ORFNames=UNG524/PRO1066; Homon Ghrand (Human)
Homo sapiens (Human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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(c) 1993 - 2005 Compugen Ltd
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GGHEL HUMAN
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GGUBZ - MACMU
G5 Y 39 2 HUMAN
GHRL FELCA
GHRL FELCA
GHRL GANFA
OTTSD1 MOUSE
GHRL RAT
OF SEL RANTA
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Maximum Match 100%
Listing first 45 summaries
                                                                                                            protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
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135.5
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122.5
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Perfect score:
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Jeffery P. L., Herington A.C., Chopin L.K.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
Expect AY184207, AAQ27351.1; -; mRNA.
R EMBL; AY18420700157017, Homo sapiens.
R GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA.
R GO; GO:0016091; P:requiation of physiological process; IEA.
InterPro; IPRO05738; motilin ghrelin.
R PANTHER; PTHR1422; Preproghrelin.
R PANTHER; PTHR1422; Preproghrelin; 1.
R PANTHER; POUGL4; Motilin ghrelin; 1.
R Pfan; PF04644; Motilin ghrelin; 1.
R PRINTS; PR01624; GHRELIN.
C SEQUENCE 91 AA; 9972 MW; E7ES32D32A3F8609 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Exon 3-deleted preproghrelin variant.
Homo saplens (Human).
                                        OGVWJG ANAPL
OS2856 BACSU
OS2856 TETNG
ORSAUL YERPE
OG6549 YERPS
O9W201 DROME
O4WHI8 ASPFU
SNX41 EMENI
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Q6V501 RABIT
Q5P090 AZOSE
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Q8GYPB;
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Pubmed=12414809, DOI=10.1074/jbc.M205366200,
Hosoda H., Kojima M., Mizushima T., Shimizu S., Kangawa K.;
Hosoda H., Kojima M., Mizushima T., Shimizu S., Kangawa K.;
Structural divergence of human ghrelin. Identification of multiple
ghrelin-derived molecules produced by post-translational processing.";
J. Biol. Chem. 278:64-70(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).

MEDLINE-22887296; PubMed=12975309; DOI=10.1101/gr.1293003;

Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,

Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,

Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,

Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,

Lewis L., Liso D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,

Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,

Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,

Wood W.I., Godowski P.J., Gray A.M.;

The secreted protein discovery initiative (SPDI), a large-scale

effort to identify novel human secreted and transmembrane proteins: a
                                                                                                                                                                                     NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROTEIN SEQUENCE OF 24-33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2), TISSUE SPECIFICITY, ACYLATION OF SER-26, AND MASS SPECTROMETRY.
                                                                           Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K., "Ghrelin is a growth-hormone-releasing acylated peptide from
                                                                                                                                                                                                                                           Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O., Staub A., Alexander G., Chenard M.-P., Rio M.-C.; "Identification and characterization of a novel gastric peptide hormone: the motilin-related peptide."; Gastroenterology 119:395-405 (2000).
                   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND ACYLATION OF SER-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                      TISSUE-Stomach; MEDLINE-20067959; PubMed=10604470; DOI=10.1038/45230;
                                                                                                                                                                                                                                                                                                                                                                                          Wajnrajch M.P., Ten I.S., Gertner J.M., Leibel R.L., "Genomic organization of the human Ghrelin gene."; J.* Endocr. Genet. 1:231-233(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
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                                                                                                                                                                                                         TISSUE=Stomach;
MEDLINE=20389976; Pubmed=10930375;
                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bioinformatics assessment.";
Genome Res. 13:2265-2270(2003).
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                                                                                                                                          Nature 402:656-660(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Stomach;
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R. Pander-13310161, DOI-10.1110/pss.04682504;
R. Pander-13310161, DOI-10.1110/pss.04682504;
R. Pander-13310161, DOI-10.1110/pss.04682504;
R. Pander-13310161, DOI-10.110/pss.04682504;
R. Pander-13310161, Doi-10.110/pss.04682504;
R. Pander-13010161, Doi-10.110/pss.04682504;
R. Lander-13010161, R. Rader-13010161, R. Rader-1
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Name=GHRL;
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SEQUENCE
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                                                                                                                                     Ghrelin-28.
Ghrelin-27.
Ghrelin-27.
O-decanoyl serine (in form ghrelin-27-C10 and form ghrelin-28-C10).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Angeloni S.V., Glynn N., Ambrosini G., Garant M.J., Dee Higley J., Angeloni S.V., Glynn N., Ambrosini G., Garant M.J., Dee Higley J., Angeloni S.V., Glynn N., Ambrosini G., Garant M.J., Dee Higley J., Angertation of the rhesus monkey ghrelin gene and factors influencing ghrelin gene expression and fasting plasma levels."; Endocrinology 145:2197-2205 (2004).

E Rembl., ANY12274, AAQ74837.1: -, Genomic_DNA.

E RMBL, ANY12275, Cestracellular region, IEA.

R GO, GO:0005678; Figrowth hormone-releasing hormone activity; IEA.

GO, GO:0016608; Figrowth hormone-releasing hormone activity; IEA.

R GO, GO:0050791; P:regulation of physiological process; IEA.

InterPro; IPR006738; motilin ghrelin.

InterPro; IPR005738; motilin ghrelin.
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Cercopithecidae; Cercopithecinae; Macaca.
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Pfam, PF04644; Motilin_ghrelin; 1.
PRINYS; PRO1624; GHRELIN.
PPCDOm; PD332162; Preproghrelin; 1.
3D-structure; Alternative splicing; Direct protein sequencing;
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 117;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Score 198; DB 1; Length 11
Pred. No. 1.4e-12;
0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                        form ghrelin-28).
Missing (in isoform 2).
//TId-Vgp 003245.
i. -> M (in Ref. 6).
4; 39C0572EBECA2755 CRC64;
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Pfam; PF04644; Motilin_Ghrelin; 1.

PRINTS; PR01624; GHRELIN.

PRODOM; PD32122; Prepredhrelin; 1.

SEQUENCE 117 AA; 12913 MW; 1B634ACE1E1F19FF CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
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                                                                                            Hormone, Lipoprotein, Signal.
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QGUDE7;
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Best Local Similarity 88.6
Marches 39, Conservative
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MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRAQQRKESKKP 44

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$5-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
35-OCT-2004 (TremBlrel. 28, Last annotation update)
Ghrelin (Fragment).
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Name=2; Synonyms-del-Gln14-ghrelin;
Isoid=Q6BEG6-2; Sequence-VSP 011626;
PTM: O-n-octanoylation is essential for activity (By similarity).
SIMILARITY: Belongs to the motilin family.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Felidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lin X., Miyazato M., Kaiya H., Ida T., Kangawa K.;
"cDNA cloning of feline and caprine ghrelin.";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Specific ligand for the growth hormone secretagogue receptor type 1 (GHSR) inducing the release of growth hormone the pituitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in growth regulation (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                     promoters.";
Endocrinology 146:1611-1625(2005).
Endocrinology 146:1611-1625(2005).
EMBL; AR701846; AAU93610.1; -; Genomic_DNA.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA.
InterPro; IPR00541; Preproghrelin.
PANTHER; PTHR14122; Preproghrelin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-OCT-2004 (Rel. 45, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                               NUCLECTIDE SEQUENCE.
PubMed=15604212; DOI=10.1210/en.2004-1306;
Wei W., Wei W., Weng G., Qi X., Englander E.W., Greeley G.H. Jr.;
"Characterization and regulation of the rat and human ghrelin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 AA; 3887 MW; BEAF2F6ABD6968BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing, Named isoforms=2;
Name=1; Synonyms=Ghrelin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30.2%; Score 187; DB 2; I 100.0%; Pred. No. 4.6e-12; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQ 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQ 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2
QSY392_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 36; Conserv
                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Stomach;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GHRL FELCA
Q6BEG6; Q6BEG5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Felinae; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ++
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
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                        between the Swiss Institute of Bioinformatics and the EMBL outetation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
Swiss-Prot entry is copyright. It is produced through a collaboration
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"cDNA cloning of feline and caprine ghrelin.";
Submitted (JUL-2002) to the EMBL/GenBank/DDB databases.
-!- FUNCION: Specific ligand for the growth hormone secretagogue receptor type I (GHSR) inducing the release of growth hormone from the pituitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in growth regulation (By shillarity).
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTM: O-n-octanoylation is essential for activity (By similarity). SIMILARITY: Belongs to the motilin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              By similarity.
Ghrelin (By similarity).
Removed in mature form (By similarity).
O-octanoyl serine (By similarity).
Missing (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Capra hircus (Goat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
Pecora, Bovidae, Caprinae, Capra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Growth hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 180; DB 1; Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MPSPGTVCSLLLFSMLWADLAMAGSSFLSPEHQKVQQRKESKKP 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 AA; 12956 MW; 8235A51447FFF530 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lipoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-OCT-2004 (Rel. 45, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
11-SEP-2005 (Rel. 48, Last annotation update)
Ghzelin precursor (Growth hormone secretagogue)
releasing peptide) (Motilin-related peptide).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                          EMBL; AB089201; BAD34670.1; -; mRNA.
EMBL; AB089202; BAD34671.1; -; mRNA.
InterPro; IPR006739; motilin_assoc.
InterPro; IPR006739; motilin_assoc.
InterPro; IPR006734; preproghrelin.
PANTHER; PTHR14122; Preproghrelin; 1.
PAM, PF04643; Motilin_assoc; 1.
Pfam; PF04644; Motilin_assoc; 1.
Pfam; PR04644; Motilin_assoc; 1.
Promom; PR04644; Motilin_ghrelin; 1.
Probom; PR032162; Preproghrelin; 1.
Alternative splicing; Hormone; Lipoprote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=VSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB089200; BAD34669.1; -; mRNA.
InterPro; IPR006737; motilin_assoc.
InterPro; IPR006738; motilin_ghrelin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9925;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               снкь сарні
Обвеб7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=GHRL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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PROPEP
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                                                                                                                                     removed.
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   This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAPHVVPALPLSNQL-CDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22; Gaps
                                                                                                                                                                                                                                                                                                                                           Ghrelin (By Similarity).
Removed in macure form (By similarity).
O-octanoyl Serine (By similarity).
CDA67971D72E3303 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.7%; Score 171.5; DB 1; Length 116; 42.9%; Pred. No. 7.6e-10; ive 13; Mismatches 34; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.6%; Score 165; DB 2; Length 117; 41.0%; Pred. No. 3.7e-09; ive 8; Mismatches 32; Indels 3
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SEQUENCE 117 AA; 13035 MW; 27657687FC026A74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 EQQRH-----LWASVESQSTXDSGSDLTVSGRTWG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GSQEEGAEDELEIRFNAPFNIGIKLSGAQSLQHGQTLG 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 AA
                                                                                                                                                                                                                                                                                                            By similarity
InterPro; IPR005441; Preproghrelin.
PANTHER, PTHR4122; Preproghrelin; 1.
Pfam; PF04643; Motilin_assoc; 1.
Pfam; PF04644; Motilin_ghrelin; 1.
PRINTS; PR01624; GHRELIN.
ProDom; P3032162, Preproghrelin; 1.
Hormone; Lipoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PANTHER; PTHR14122; Preproghrelin; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF04643; Motilin assoc; 1.
Pfam; PF04644; Motilin ghrelin; 1.
PRINTS; PR01624; GHRELIN.
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NCBI_TaxID=10047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 AA; 12935 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 41.0%;
nes 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 42.9%
Matches 42; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ghrelin preproprotein.
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PEPTIDE
PROPEP
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Thu Dec 22

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RA MEDLINEZ2359519; Furned M. Kasukwa T., Adachi J., Bono H., Kondo S., RA Vikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Rayai K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Golobori T., Baldarelli R., Hill D.P., Matsuda H., Schonbach C., Golobori T., Baldarelli R., Hill D.P., Matsuda H., Batalov S., Beisel K.W., RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Blake J.A., Ranadha T.A., Fletcher C.F., Forzet A., Frazer K.S., Gasteriad T., Gariboldi M., Gissi C., Godzik A., Gough J., RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Ranaj A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., RA Maglott D.R., Malteis L., Marchionni L., McKenzie L., Miki H., RA Maglott D.R., Malteis L., Marchionni L., McKenzie L., Miki H., RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., Petrovoky N., Pillai R., Ponicius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Ravardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells R. Hurozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K., Rawai J., Azawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Sabaka R., Shiragawa I., Rayasaki A., Sasaki K., Sasaki D., Shibata K., Ishingawa A., Hara A., Hashizume W., Imotani C., Shander E.S., Rogers J., Paranaki M., Sasaki M., Sasaki D., Shibata K., Shinagawa A., Rannaki M., Waterston R., Lander E.S., Rogers J., R., Rannaki M., Waterston R., Lander E.S., Rogers J., R., Rannaki M., Waterston R., Lander E.S., Rogers J., R., Rannaki M., Waterston R., Lander E.S., Rogers J., R., Rannaki M., Waterston R., Lander E.S., Rogers J., R., Rannaki M., Rannaki M.,
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"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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:
                                                                                                                                                                                           Name-Ghrī; Synonyme-Wirp;
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE (GENOMIC DNA) (ISOFORM 1).
Tanaka M., Hayashida Y., Iguchi T., Nakao N., Nakai N., Nakashima K.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEVELOPMENTAL STAGE, AND ACYLATION OF SER-26.
PubMed=1574625; DOJ=10.1210/en.2004-0645.
Nibhi Y., Hiejima H., Mifune H., Sato T., Kangawa K., Kojima M.;
"Developmental changes in the pattern of ghrelin's acyl modification
                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE (MRNA) (ISOFORMS 1 AND 2), PROTEIN SEQUENCE OF 24-30, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY. TISSUE-Stomach;
                                         09EQX6; Q9WUZ1;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2005 (Rel. 41, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (M46 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O., Staub A., Alexander G., Chenard M.-P., Rio M.-C.; "Identification and characterization of a novel gastric peptide hormone: the motilin_related peptide.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CS7BL/60; TISSUE=Stomach; MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kojima M.;
"Mouse mRNA for preproghrelin.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
                           117 AM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gastroenterology 119:395-405(2000).
                           PRT;
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                           STANDARD;
                           GHRL_MOUSE
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GHRL_MOUSE
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Name=1; Synonymas-Girelin; Synonymas-Girelin; Isola-QPBCXV0-1; Sequence-Displayed;
Isola-QPBCXV0-1; Sequence-Displayed;
Name=2; Synonymas-Girelin-Girelin; Isola-QPBCXV0-2; Sequence-USP 003246;
-1- TISSUE SPECIFICITY: Mainly expressed in the gastrointestinal tract with higher levels in the stomach, medium levels in the duodenum, jejunum, ileum and colon. Low expression in the testis and brain. Not detected in the salivary gland, pancreas, liver and lung.
-1- DFVELOPHENTAL STAGE: Levels of n-octanoylated and n-decanoylated ghrelin drop by one third and 3-fold, respectively, between postnatal weeks 3 and 4 due to change of diet during weaning.
-1- PTM: O-n-octanoylated form ghrelin-Cio differs in the length of the carbon backbone of the carboxylic acid bound to Ser-26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              European Bioinformatics Institute. There are no restrictions on its as long as its content is in no way modified and this statement is not
                                                                                                                                                                                               hormone secretagogue receptor.";
Trends Endocrinol. Metab. 12:118-122(2001).
-!- FUNCTION: Specific ligand for the growth hormone secretagogue receptor type 1 (GHSR) inducing the release of growth hormone from the pituitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in
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                                                                                   REVIEW.
MEDINE=21203998; PubMed=11306336; DOI=10.1016/S1043-2760(00)00362-3;
Kojima M., Hosoda H., Matsuo H., Kangawa K.;
"Ghrelin: discovery of the natural endogenous ligand for the growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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O-octanoyl serine (in form n-octanoyl
ghrelin).
Missing (in isoform 2).
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and the levels of acyl-modified ghrelins in murine stomach.";
Endocrinology 146:2709-2715(2005).
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Pred. No. 5.9e-09;
7; Mismatches 33; Indels 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 AA; 13207 MW; EACB49DZE3CA7203 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=2;
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EMBL; AB035701; BAB19046.1; -; mRNA.
EMBL; AB060078; BAB69857.1; -; Genomic_DNA.
EMBL, AK008658; BAB25814.1; -; mRNA.
EMBL, AK008660; BAB25344.1; -; mRNA.
ERNBE., AK008660; BAB25344.1; -; mRNA.
ERNBE.MISCO000064177; MUS musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0005737; C:cytoplasm; IDA.
GO; GO:0005615; C:extracellular space; TV
GO; GO:0005179; F:hormone activity; TAS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro, IPR006737; motilin_assoc.
InterPro, IPR006738; motilin_ghrelin.
InterPro, IPR005441; Preproghrelin.
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Pfam; PF04643; Motilin assoc; 1.
Pfam; PF04644; Motilin ghrelin; 1.
                                                                                                                                                                                                                                                                                                                                                                             growth regulation.
SUBCELLULAR LOCATION: Secreted.
ALTERNATIVE PRODUCTS:
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Probom: process constants
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A Jeffery P.L., Duncan R.P., Yeh A.H., Jaskolski R.A., Hammond D.S., Jeffery P.L., Duncan R.P., Yeh A.H., Jaskolski R.A., Hammond D.S., Herington A.C., Chopin L.K., Yeh A.H., Jaskolski R.A., Hammond D.S., Tepression of the ghrelin axis in the mouse: an exon 4-deleted mouse proghrelin variant encodes a novel C terminal peptide."; Endocrinology 146:432-440(2005).
REMBL; AX177430; AA027350.1; AMNA.
REMBL; AX177430; AA027350.1; Mus musculus.
RGJ; MGI:1930008; Ghrl.
RGJ; GO:000513; C:cytoplasm; IDA.
RGO; GO:0005179; Fibramone activity; TAS.
RJ GO; GO:00179; Fibramone activity; TAS.
RINTERPRO; IPRO06738; motilin ghrelin.
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           MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAPHVVPALPLSNQLCDLE
                       1 MLSSGTICSLILLSMLWMDWAMAGSSFLSPEHQKAQQRKESKKP-----PAKLQPRALE
                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
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                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GHRL CANFA STANDARD; PRT; 11, AA. Q9BEF8, Q9BEF9; 11, Created)
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Ghrelin precursor (Growth hormone secretagogue)
releasing peptide) (Motilin-related peptide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 162; DB 2;
Pred. No. 5.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE (MRNA) (ISOFORMS 1 AND 2).
                                                                                                                                     86 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.1%; Scor. 70.5%; Pred. No. 5...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PANTHER, PTHR14122; Prepredictin; 1. Pfam; PF04644; Motilin ghrelin; 1. PRINTS; PR01624; GHRELIN.
                                                                                                                                                          (TrEMBLrel. 24, Created) (TrEMBLrel. 24, Last seq
                                                                                                                                                                                01-MAR-2004 (TrEMBLrel. 26, Last ann
Exon 4-deleted preproghrelin variant
                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=GHRL; Synonyms=MTLRP;
Canis familiaris (Dog).
                                                                                                                                     QB11T4 MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Gastric fundus;
                                                                                                                                                                                                     Name=Ghrl;
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
es 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                STRAIN=Swiss;
                                                                                                                                                           01-JUN-2003
                                                                                                                                                                       01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
                                                                                                              셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isola=09BER8-1; Sequence-Displayed;
Name=2; Synonyms=del-Gln14-ghrelin;
Isolae09BER8-2; Sequence=VSP_001244;
PTM: O-n-cottanoylation is essential for activity (By similarity).
SIMILARITY: Belongs to the motilin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ghrelin delta2.
Name=Ghrl; Synonyms=Ghrelin;
Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            By similarity.

Ghrelin (By similarity).

Ghoctanoyl serine (By similarity).

O-octanoyl serine (By similarity).

Missing (in isoform 2).

Fride-VSP_002244.
                                                                                                                                                                                                                                   "Dog ghrelin.";
Submitted (APR-2001) to the EWBL/GenBank/DDBJ databases.
-!- FUNCTION: Specific ligand for the growth hormone secretagogue receptor type 1 (GHSR) inducing the release of growth hormone the pituitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in growth regulation (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
Tomasetto C., Wendling C., Rio M.-C., Poitras P.; "Identification of cDNA encoding MTLRP/ghrelin precursor from dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                      NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
TISSUE-Stomach;
Doi K., Kojima M., Hosoda H., Kaiya H., Matsuo H., Kangawa K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MPSLGTWCSLLLFSVLWVDLAMAGSSFLSPEHQKLQQRKESKKP 44
                                                                                  Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AJ298255; CAC29155.1; -; mRNA.
EMBL; AJ298296; CAC29156.1; -; mRNA.
EMBL; AJ298296; CAC29156.1; -; mRNA.
ENSEL; AB060700; BAC75929.1; -; mRNA.
ENSEMBL; ENSCAFGO0000005529; Canis familiaris.
InterPro; IPR006737; motilin_assoc.
InterPro; IPR006738; motilin_ghrelin.
InterPro; IPR005441; Preproghrelin.
PANTHER, PTHR14122; Preproghrelin; 1.
Pfam; PF04643; Motilin_assoc; 1.
Pfam; PF04644; Motilin_assoc; 1.
Pfam; PR04644; Motilin_ghrelin; 1.
PRINTS; PR01624; GHRELIN.
Probom; P3332162; Preproghrelin; 1.
Probom; P3332162; Preproghrelin; 1.
Alternative splicing; Hormone; Lipoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 AA; 13007 MW; 3E57FED9D1847CF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=2;
Name=1; Synonyms=Ghrelin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 162; DB 1;
Pred. No. 7.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 AA
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70.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q7TSD1 MOUSE PRELIMINARY;
Q7TSD1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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51
117
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   .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAPHVVPALPLSNQLCDLE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MLSSGTICSLLLLSMLWMDMAMAGSSFLSPEHQKAQFNAP-----FPDVGIKLSGAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHARACTERIZATION.
MEDLINE=21092536; PubMed=11162448; DOI=10.1006/bbrc.2000.4039;
Hosoda H., Kojima M., Matsuo H., Kangawa K.;
"Ghrelin and des-acyl ghrelin: two major forms of rat ghrelin peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hosoda H., Kojima M., Matsuo H., Kangawa K.;
"Purification and characterization of rat des-Gln14-ghrelin, a second
endogenous ligand for the growth hormone secretagogue receptor.";
J. Biol. Chem. 275:21995-22000(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), PROTEIN SEQUENCE OF 24-51, MASS SPECTROMETRY, AND ACYLATION OF SER-26.
STRAIN=Sprague-Dawley; TISSUE-Stomach;
MEDLINE=20067959; Pubmed=10604470; DOI=10.1038/45230;
Kojima M., Hosoda H., Date Y., Nakazato M., Mateuo H., Kangawa K.;
"Ghrelin is a growth-hormone-releasing acylated peptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Growth hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-51, MASS SPECTROMETRY, AND ACYLATION OF SER-26.
STRAIN-Sprague-Dawley, TISSUE-Stomach;
MEDLINE-20357315; PubMed=10801861; DOI=10.1074/jbc.M002784200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                       Hisatomi H., Nagao K., Hirata H., Kawano K., Hibi N.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AB111891; BAC77409.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PD332162; Preproghrelin; 1.
3 78 AA; 8615 MW; AD87CB53C9A22FFB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in gastrointestinal tissue.";
Biochem. Blophys. Res. Commun. 279:909-913(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O9QYH7; Q9ET69;
28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Ghrelin precursor (Growth hormone secretagogue)
releasing peptide) (Motilin-related peptide).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;; Pred. No. 1.1e-08;
11; Mismatches 18
                                                                                                                                                                                                                                                                     GO; GO:0005737; C:Cytoplasm; IDA.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0005179; F:hormone activity; TAS.
InterPro; IPR005437; motilin_assoc.
InterPro; IPR005441; Preproghrelin.
PANTHER; PTHR14122; Preproghrelin; 1.
PRINTS; PR01643; Metilin_assoc; 1.
PRINTS; PR01624; GHRELIN.
ProDom; PD332162; Preproghrelin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:| | | :: :| | 52 YQQHGRALGKFLQDILWEEV----KEAPAD 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 QORH-----LWASVFSQSTKDSGSD 80
                                                                                                                                                                                              Ensembl; ENSTUS G0000064177; Mus musculus. MGI; MGI:1930008; Ghrl. G0; GO:0005737; C:CVEODISSM: Tha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.6%; Score 158.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 40.7% nes 37, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 402:656-660(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
   Muridae; Murinae; Mus.
                                                                                          NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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OC REPRESENTATION OC STATE OF 
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GO; 03.0005615; C:extracellular space; IC.
GO; GO:0001664; F:G-protein-coupled receptor binding; IPI.
GO; GO:00016608; F:growth hormone-releasing hormone activity; IDA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IDA.
GO; GO:000718; P:G-protein coupled receptor protein signalin. .; IDA.
GO; GO:0050791; P:regulation of physiological process; NAS.
InterPro; IPR006737; motilin_ghrelin.
InterPro; IPR006441; Preproghrelin.
InterPro; IPR00441; Preproghrelin; 1.
PANTHER; PTHR14122; Preproghrelin; 1.
Pfam; PF04643; Motilin_ghrelin; 1.
Pfam; PF04644; Motilin_ghrelin; 1.
Pfam; PF04644; Motilin_ghrelin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hormone secretagogue receptor.";
Trends Endocrinol. Metab. 12:118-122(2001).
-!- FUNCTION: Specific ligand for the growth hormone secretagogue receptor type 1 (GHSR) inducing the release of growth hormone from the pituitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD332162; Preproghrelin; 1.
Alternative splicing; Direct protein sequencing; Hormone; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISOId=09QYH'-1; Sequence=Displayed;
Name=2; Synonyms=del-Gln14-ghrelin;
Isoid=09QYH'-1; Sequence=VSP 003248;
Isoid=09QYH'-1; Sequence=VSP 003248;
Isoid=09QYH'-1; Sequence=VSP 003248;
Isoid=09QYH'-2; Sequence=VSP 003248;
Isoid=09QYH'-2; Sequence=VSP 003248;
Intesting are detected in the hypothalamus, heart, lung, pancreas, intesting and adipose tissue.
In PTM: O-n-octanoylation is sesential for activity. The replacement of Ser-26 by aromatic tryptophan preserves ghrelin activity.
NASS SPECTROMETRY: MW=3314.9; MW ERR=0.7; METHOD=Electrospray;
NASS SPECTROMETRY: MW=3187.1; MW ERR=0.6; METHOD=Electrospray;
NASS SPECTROMETRY: MW=3187.1; MW ERR=0.6; METHOD=Electrospray;
INIMARITY: Belongs to the motilin family.
                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                           [5]
REVIEW.
MEDLINE=21203998; PubMed=11306336; DOI=10.1016/S1043-2760(00)00362-3;
[4]
STRUCTURE.ACTIVITY RELATIONSHIP.
MEDLINE=21433488; PubMed=11549267; DOI=10.1006/bbrc.2001.5553;
MALSHUMOLO M., Hogoda H., Kitajima Y., Morozumi N., Minamitake Y.,
Tanaka S., Matsuo H., Kojima M., Hayashi Y., Kangawa K.;
"Structure-activity relationship of ghrelin: pharmacological study
                                                                                                                                                                                                                                                                                                                                                                                                    Kojima M., Hosoda H., Matsuo H., Kangawa K.;
"Ghrelin: discovery of the natural endogenous ligand for the growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW; 8857546FE51A7691 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Removed in mature form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splitting, Named isoforms=2;
Name=1; Synonyms=Ghrelin;
                                                                                                                                                                                                                        ghrelin peptides.";
Biochem. Biophys. Res. Commun. 287:142-146(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; B59316; B59316.
Ensembl; ENSRNOG0000010349; Rattus norvegicus.
RGD; 632283; Ghrl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O-octanoyl serine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB029433; BAA89370.1; -; mRNA.
EMBL; AB035699; BAB11956.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            growth regulation.
-!- SUBCELLULAR LOCATION: Secreted.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13176
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51
117
26
37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24
52
37
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Length 117;

DB 1;

Score 158;

25.5%;

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EMBL; AB035703; BAB19048.1; -; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sus scrofa (Pig).
Eukaryota, Metazoa;
Mammalia, Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9823;
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Stomach;
                                       NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               removed.
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SO DR PRESENTATION OF THE PRESENT AND DR PRESENTATION OF THE PRESE
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                                                                                                    54
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                                                                                                       1 MVSSATICSLILLSMLWMDWAWAGSSFLSPEHOKAQORKESKKP-----PAKLOPRALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAPHVVPALPLSNQL-CDL
                        22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                    Preproghrelin precursor.
Ovis aries (Sheep).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB06609; BAC75928.1; -; mRNA.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:000576; C:extracellular region; IEA.
GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA.
GO; GO:0050791; P:regulation of physiological process; IEA.
InterPro; IPR066737; motilin_ghrelin.
InterPro; IPR065738; motilin_ghrelin.
PANTHER; PTHR14122; Preproghrelin;
PERM; PF04644; Motilin_ghrelin; 1.
PERM; PF04644; Motilin_ghrelin; 1.
PERM; PF04644; Motilin_ghrelin; 1.
PERM; PF04644; Motilin_ghrelin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Doi K., Kojima M., Hosoda H., Kaiya H., Matsuo H., Kangawa "sheep ghrelin.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                              61 QQRH-----LWASVFSQSTKDSGSDLTVSGRTWG 89
                                                                                                                                                                             40.0%; Pred. No. 2e-08;
iive 7; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.4%; Score 157.5; DB 2; Length 40.8%; Pred. No. 2.2e-08; ive 14; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ghrelin.
B78ECA3DBF0E568E CRC64;
                                                                                                                                                                                                                                                                                                                                      01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 EQQRH-----LWASVFSQSTKDSGSDLTVSGRTWG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD332162; Preproghrelin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pecora; Bovidae; Caprinae; Ovis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 gl
12977 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q67BB5 PIG PRELIMINARY;
Q67BB5;
25-OCT-2004 (TrEMBLrel. 28, C
25-OCT-2004 (TrEMBLrel. 28, L
25-OCT-2004 (TrEMBLrel. 28, L
Ghrelin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 25.4% Best Local Similarity 40.8% Matches 40; Conservative
                                                                                                                                                                                                                                                                                             Q863L0_SHEEP PRELIMINARY;
Q863L0;
                     42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24
116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
TISSUE=Stomach;
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
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067BBS PIG
1D 067BBS,
AC 067BBS,
DT 25-0CT-
DE 35-0CT-
DE Ghrelit
OS Sus sci
CC Bulkary
OC Bulkary
OC Sus Sus.
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                        Matches
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Isold=Q9GKX5-1; Sequence=Displayed;

Name=2; Synonyms=del-Gln14-Ghrelin;

Isold=Q9GKX5-2; Sequence-VSP 003247;

PTM: O-n-octanoylation is essential for activity (By similarity).

SIMILARITY: Belongs to the motilin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata, Craniata, Vertebrata, Euteleostomi,
Laurasiatheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rousselle J., Lacroix D., Dubreuil P.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Specific ligand for the growth hormone secretagogue receptor type 1 (GHSR) inducing the release of growth hormone the pituitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in growth regulation (By similarity).
-!- SUBCELLULAR LOCATION: Secreted (By similarity).
                                    Nim K.-S., Kotnscnild M.F.;
"Big Ghrelin.";
"Big Ghrelin.";
"Big Ghrelin.";
"Big Ghrelin.";
"Bibmitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
"BMBL; AX373019; AAR24571.1; -; Genomic_DNA.
"BMBL; AX373019; C: extracellular region; IEA.
"GO; GO:005576; C: extracellular region; IEA.
"GO; GO:005576; F: growth hormone-releasing hormone activity; IEA.
"GO; GO:0050791; P: regulation of physiological process; IEA.
InterPro; IRR00541; P: Preproghrelin.
"DANTHER; PTHR14122; Preproghrelin; 1.
"PRINTS; PRO4644; Motilin. ghrelin; 1.
"PRINTS; PRO4644; GRELIN.
"A4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OGGKT5; Q9BDG8; Q9GK4; L18 AA.
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KOjima M.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MPSPGTVCSLLLLGMLWL-DLAMAGSSFLSPEHQRVQVRPPHKAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MPSIGTICSLLLLSVLLMADLAMAGSSFLSPEHQKVQQRKESKKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 AA; 7980 MW; 875424C2D41FC166 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing, Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 150.5; DB 2
Pred. No. 6.8e-08;
4; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.3%;
SEQUENCE.
Rothschild M.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32; Conservative
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DR EMBL; AB035704; BAB19049.1; -; mRNA,

EMBL; AF208930; AAK19243.1; -; mRNA,

EMBL; A7028942; AAK30002.1; -; mRNA,

BR InterPro; IPR006737; motilin_dasor.

InterPro; IPR006737; motilin_dhrelin.

DR InterPro; IPR006738; motilin_dhrelin.

DR Pfam; PP04643; Motilin_dhrelin.

DR Pfam; PP04644; Motilin_dhrelin.

DR Pfam; PP04644; Motilin_dhrelin.

DR Probom; PD332162; Preproghrelin; 1.

DR PRNTS; PR01624; GHRELIN.

DR PROPER 1 24 Ghrelin.

FT SGNAL 1 24 Ghrelin.

FT SGNAL 25 52 Ghrelin.

FT PR0PER 53 118 Removed in mature form (By similarity).

FT CONFLICT 38 38 7 Ghrelin.

FT CONFLICT 17 17 17 L-PE (in Ref. 2; AAK30002).

FT CONFLICT 72 72 K -> E (in Ref. 2; AAK30002).

FT CONFLICT 17 17 17 L-PE (in Ref. 2; AAK30002).

FT CONFLICT 17 17 17 L-PE (in Ref. 2; AAK30002).

SQ SEQUENCE 118 AA; 12786 MM; 85603E1D6DABLA76 CRC64;

AQUETY MATCH 24.3%; Score 150.5; DB 1; Length 118;

Best Local Similarity 71.1%; Pred. No. 1.2e-07;

MASTOTICSLILLGMLML-DLAMAGSSFLSPEHQRVQORKESKKP 45

DD 1 MPSTOTICSLILLGYLML-DLAMAGSSFLSPEHQRVQORKESKKP 45
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Search completed: December 21, 2005, 13:39:53 Job time : 230 secs

initis ruye biank (uspto)

Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 23944, A Sequence 6, Appli Sequence 1255, Ap Sequence 27822, A Sequence 27822, A Sequence 27822, Ap Sequence 34, Appli Sequence 34, Appli

Title: Perfect score:

Run on:

Sequence:

Searched:

```
Query Match 31.9%; Score 198; DB 2; Length 117; Best Local Similarity 88.6%; Pred. No. 4e-17; Matches 39; Conservative 0; Mismatches 5; Indels
                                               US-08-454-121A-3
US-08-454-121A-3
US-09-057-951A-2
US-09-057-991A-23944
US-08-391-916A-8
US-08-391-916A-8
US-10-104-047-3255
US-09-252-991A-27892
US-09-252-991A-27892
US-09-224-66-2
5340934-13
US-08-990-511-34
US-08-990-511-34
US-08-528-134
US-08-528-134
US-08-528-134
US-08-528-134
US-08-528-134
US-08-528-134
US-09-528-134
US-09-528-134
US-09-528-134
US-09-528-134
US-09-569-108A-34
US-09-569-108A-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTE: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastERO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/046,479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09046479;
Patent No. 6291653;
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Deisher, Theresa A.
TITLE OF INVENTION: WOTLIN HOMOLOGS
CORRESPONDENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY, AGBNT INFORMATION:
NAME: SAW! Black, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 97-04
TELECOMMUNICATION INFORMATION:
TELECHONE: 206-442-6672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 117 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 206-442-6678
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MOLECULE TYPE: protein
FRAGMENT TYPE: internal
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  Sequence 4, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 268, App
Sequence 1, Appli
Sequence 17248, A
Sequence 17248, A
Sequence 1748, A
Sequence 1748, A
Sequence 17513, A
Sequence 1569, A
Sequence 1748, A
Sequence 1748, A
Sequence 17513, A
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Sequence 17387, A
Sequence 4470, Ap
Sequence 3, Appli
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                                                                                                                                                                                     December 21, 2005, 13:32:33 ; Search time 46 Seconds (without alignments) 210.284 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                620
1 MPSPGTVCSLLLLGMLWLDL......PPSSRERSRRSHQPSCSPEL 117
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2: /cgn2 6/ptodata/1/iaa/6 COMB.pep:*
3: /cgn2 6/ptodata/1/iaa/H COMB.pep:*
4: /cgn2 6/ptodata/1/iaa/PCTUS COMB.pep:*
5: /cgn2 6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2 6/ptodata/1/iaa/RE_COMB.pep:*
                              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-104-047-3650
PCT-US95-04910-14
US-09-252-991A-17387
US-09-134-000C-4470
US-08-489-666C-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fotal number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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31.9%; Score 198; DB 2; Length 117;
Best Local Similarity 88.6%; Pred. No. 4e-17;
Matches 39; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                       DB 2; Length 117;
                                                                                                                                                                                                                                                                                       Query Match 31.9%; Score 198; DB 2; Length 11 Best Local Similarity 88.6%; Pred. No. 4e-17; Matches 39; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 44
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INCOGRAPTION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Deisher, Theresa A.
APPLICANT: Deisher, Theresa A.
APPLICANT: Deapers, Stephen R.
FITLE OF INVENTION: TML PEPTIDES
FILE REFERENCE: 97-04C1
CURRENT APPLICATION UNDBER: US/09/404,417A
CURRENT FILING DATE: 1999-09-23
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO EBROTH: 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
PRIOR APPLICATION NUMBER: 60/141,592
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09794987
Patent No. 6838438
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
TITLE OF INFORTION: MOLIGES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09404417A
Patent No. 6627729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Seattle STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                 ; NAME/KEY: SIGNAL
; LOCATION: (1)...(23)
US-09-608-810A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-404-417A-2
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                                                                                                                                                                                      FEATURE:
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                                      1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 44
                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIANE
SOFTWARE: FSB4LSC for Windows Version 2.0
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/822,897C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-00-608-810A-4

Sequence 4, Application US/09608810A

Sequence 4, Application US/09608810A

Setent No. 6420521

GENERAL INFORMATION:

APPLICANT: Sheppard, Paul O.

APPLICANT: Dessher, Theresa A.

APPLICANT: Bishop, Paul D.

TITLE OF INVENTION: SGIP PEPTIDES

FILE REFERENCE: 99-51

CURRENT APPLICATION NUMBER: US/09/608,810A

CURRENT FILING DATE: 2000-06-30
                                                                                                                                                    Sequence 2, Application US/08822897C
Patent No. 6380158
GENERAL INPORMATION:
APPLICANT: Beigher' Fheresa A.
TITLE OF INVENTION:
MUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
                                                                                                                                                                                                                                                                                                       STREET: 1201 Eastlake Avenue East CITY: Seattle STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFRENCE/DOCKET NUMBER: 97-04
TELECOMMUNICATION INFORMATION:
TELECHONE: 206-442-6672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 117 amino acida
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 88.6
Matches 39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
FRAGMENT TYPE: internal
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PRIOR APPLICATION DATA:
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                                                                                                                                              US-08-822-897C-2
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P.73091C53
CURRENT APPLICATION NUMBER: US/09/991,181
CURRENT FILING DATE: 2001-11-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR PELLING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
PRIOR PELLING DATE: 1997-10-17
PRIOR PELLING DATE: 1997-10-17
PRIOR PELLING DATE: 1997-10-17
PRIOR PELLING DATE: 1997-11-12
PRIOR PELLING DATE: 1997-11-12
PRIOR PELLING DATE: 1997-11-12
PRIOR PELLING DATE: 1997-11-12
PRIOR PELLING DATE: 1997-11-13
PRIOR PELLING DATE: 1998-03-20
PRIOR PELLING DATE: 1998-05-08
PRIOR PELLING DATE: 1998-05-08
PRIOR PELLING DATE: 1998-05-08
PRIOR PELLING DATE: 1998-05-07
PRIOR PELLING DATE: 1998-05-08
PRIOR PELLING DATE: 1998-05-08
PRIOR PELLING DATE: 1998-05-09
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Grimaldi, J. Christopher
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Paoni, Nicholas F.
Roy, Margaret Ann.
Stewart, Timothy A.
Tumas, Daniel
Wattanabe, Colin K.
William, P. Mickey
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                                                                                                                       Perrara, Napoleone
                                                                                                                                                                                                                                          Serritsen, Mary E
                                                                                                                                                                                                                                                                                                                                                                                                   Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Kljavin, Ivar J.
Napier, Mary A.
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APPLICANT:
APPLICANT:
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88.6%; Pred. No. 4e-17;
tive 0; Mismatches 5; Indels
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Sequence 2, Application US/09853253;
Sequence 2, Application US/09853253;
Setent No. 6897286;
SEREAL INCRMATION:
APPLICANT: JASPERS, STEPHEN
APPLICANT: BISHOP, PAUL
TITLE OF INVENTION: Zsig33-like Peptides
FILE REPERENCE: 00-30
CURRENT PELING DATE: 2001-05-10;
PRIOR FILING DATE: 2001-05-10;
PRIOR APPLICATION NUMBER: 60/203,300;
PRIOR FILING DATE: 2000-05-11;
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 3.0;
SEQ ID NO 2.
APPLICATION NUMBER: US/09/794,987
FILING DATE: 27-Feb-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | INFORMATION FOR SEQ ID NO: 2:
| SEQUENCE CHARACTERISTICS:
| SEQUENCE CHARACTERISTICS:
| INFORMATION OCITION: 2:
| INFORMATION OCITION OCITIO
                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/046,479
FILING DATE: -Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Sawielak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 97-04
TELECHMUNICATION INFORMATION:
TELECHONE: 206-442-6672
TELEFAX: 206-442-6678
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Matches 39, Conservative
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ORGANISM: Homo sapiens
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US-09-991-181-268
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US-09-853-253-2
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PRIOR PELICATION NUMBER: 60/08222

PRIOR PLICATION NUMBER: 60/08222

PRIOR PLICATE DATE: 1998-66-67

PRIOR PLICATION NUMBER: 60/08222

PRIOR PLICATION NUMBER: 60/08222

PRIOR PLICATION NUMBER: 60/08323

PRIOR PLICATION NUMBER: 60/08323

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PRIOR PLICATION NUMBER: 60/08324

PRIOR PLICATION NUMBER: 60/08326

PRIOR PRICATION NUMBER: 60/08326

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R FILING DATE: 1998-06-16
R APPLICATION NUMBER: 60/089514
R FILING DATE: 1998-06-16
R APPLICATION NUMBER: 60/089532
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089598
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089598
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089599
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089601
R FILING DATE: 1998-06-18
R FILING DATE: 1998-06-19
R FILING DATE: 1998-06-19
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R R FILING DATE: 1998-06-19
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R FILING DATE: 1998-06-19
R APPLICATION NUMBER: 60/090435
R FILING DATE: 1998-06-22
R APPLICATION NUMBER: 60/090435
R FILING DATE: 1998-06-23
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R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090439
R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090435
R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090449
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R APPLICATION NUMBER: 60/088826
R APPLICATION NUMBER: 60/088828
R FILING DATE: 1998-06-11
R FILING DATE: 1998-06-11
R FILING DATE: 1998-06-11
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/088876
R APPLICATION NUMBER: 60/089105
R APPLICATION NUMBER: 60/089105
R FILING DATE: 1998-06-12
R FILING DATE: 1998-06-12
R FILING DATE: 1998-06-12
R FILING DATE: 1998-06-16
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                                                    R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088742
R FILING DATE: 1998-06-10
R FILING DATE: 1998-06-10
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088824
PRINCH PR
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                                Gurney, Austin L.
                                                                    Kljavin, Ivar J.
                                                                                               Napier, Mary A.
Pan, James
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PLC27
CURRENT APPLICATION NUMBER: US/09/997,333
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88.6%; Pred. No. 4e-17;
tive 0; Mismatches
                     APPLICATION NUMBER: US/09/796,158
FILING DATE: 28-Feb-2001
CLASSIFICATION: <UNKNOWN>
                                                                 CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/046,479
FILING DATE: cUnknown>
ATORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REFERENCE/DOCKET NUMBER: 37,438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: procein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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Patent No. 6953836
GRNREAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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Godowski, Paul J.
Grimaldi, J. Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 117 amino acide
TYPE: amino acid
STRANDEDNESS: single
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TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
CURRENT APPLICATION DATA:
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Stewart, Timothy A.
Tumas, Daniel
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Paoni, Nicholas F.
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Gerber, Hanspeter
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Napier, Mary A.
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Best Local Similarity 88.6
Matches 39; Conservative
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US-09-997-333-268
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APPLICANT:
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31.9%; Score 198; DB 2; Length 117;
Best Local Similarity 88.6%; Pred. No. 4e-17;
Matches 39; Conservative 0; Mismatches 5; Indels
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Second Sec
                     PRIOR FILING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR APPLICATION NUMBER: 60/090542
PRIOR APPLICATION NUMBER: 60/090542
PRIOR PILING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090676
PRIOR APPLICATION NUMBER: 60/090676
PRIOR APPLICATION NUMBER: 60/090679
PRIOR APPLICATION NUMBER: 60/090690
PRIOR PILING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR PELING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR APPLICATION NUMBER: 60/09169
PRIOR APPLICATION NUMBER: 60/09169
PRIOR APPLICATION NUMBER: 60/09169
PRIOR APPLICATION NUMBER: 60/09169
PRIOR PELING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/09169
PRIOR APPLICATION NUMBER: 60/09169
PRIOR PELING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091639
PRIOR PELING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091639
PRIOR PELING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091639
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-03
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PRIOR FILING DATE: 1998-07-09
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ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE; Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Seattle
STATE: WA
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NUMBER	: 1997-11-12	NUMBER: 6	: 1997-11-13	NUMBER: 60	: ISS/-II-24	NOMBER: 60/0/334	NIMBED 60	. 1998-03-20	NUMBER: 60	1998-04-28	NUMBER: 60	1998-05-07	NUMBER: 6	1998-05-28	NUMBER: 60	1998-06-02	NUMBER: 60/087609	1998-06-02	NUMBER: 6	1998-06-02	NUMBER: 6	1998-06-03	NUMBER: 60	1998-06-04	NUMBER: 60/088023	O - O - O C T	1998-06-04	NIMBER: 60	1998-06-04	NUMBER: 60	1998-06-	NUMBER	1998-06-04	NUMBER: 60	1998-06-04	NUMBER: 60	LYSS-00	1998-06-05	NUMBER: 6	: 1998-06-05	NUMBER: 60	: 1998-06-05		NIMBER 60	1998-06-09	NUMBER	1998-06-10	NUMBER: 60	NIMBER	1998-06-10	NUMBER: 60	: 1998-06-10	NUMBER: 60	: 1998-06-10	NUMBER	NIMBER 60	1998-06-11	NUMBER: 6	1998-06-11	NUMBER:	: 1998-06-11 NTMBER: 60/089105	: 1998-06-12	NUMBER: 60	1998-06-16	NUMBER: 6
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PRIOR PILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/08552
PRIOR APPLICATION NUMBER: 60/08552
PRIOR PILING DATE: 1998-06-17
PRIOR PELING DATE: 1998-06-18
PRIOR PELING DATE: 1998-06-18
PRIOR PELING DATE: 1998-06-18
PRIOR PELING DATE: 1998-06-19
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PRIOR PELING DATE: 1998-06-23
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06

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R FILING DATE: 1998-03-20

R FILING DATE: 1998-03-20

R APPLICATION NUMBER: 60/083122

R APPLICATION NUMBER: 60/08450

R FILING DATE: 1998-04-28

R APPLICATION NUMBER: 60/084600

R FILING DATE: 1998-05-07

R APPLICATION NUMBER: 60/08700

R APPLICATION NUMBER: 60/087609

R APPLICATION NUMBER: 60/087609

R FILING DATE: 1998-06-02

R APPLICATION NUMBER: 60/08759

R FILING DATE: 1998-06-02

R FILING DATE: 1998-06-02

R FILING DATE: 1998-06-02
                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1998-06-03
APPLICATION NUMBER: 60/088021
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/088030
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088033
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APPLICATION NUMBER: 60/088326
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088167
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FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088217
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APPLICATION NUMBER: 60/088824
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088826
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APPLICATION NUMBER: 60/088858
FILING DATE: 1998-06-11
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FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/088876
FILING DATE: 1998-06-11
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APPLICATION NUMBER: 60/088202
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CURRENT PILING DATE: 2001-11-14

PRIOR PELLING DATE: 1997-06-16

PRIOR PELLING DATE: 1997-0-17

PRIOR PELLING DATE: 1997-10-17

PRIOR PELLING DATE: 1997-11-12

PRIOR FILING DATE: 1997-11-12

PRIOR FILING DATE: 1997-11-12

PRIOR PELLING DATE: 1997-11-13

PRIOR PELLING DATE: 1997-11-14

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31.9%; Score 198; DB 2; Length 117;
Best Local Similarity 88.6%; Pred. No. 4e-17;
Matches 39; Conservative 0; Mismatches 5; Indels
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                            PRIOR FILING DATE: 1998-0.7-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-0.7-02
PRIOR FILING DATE: 1998-0.7-02
PRIOR FILING DATE: 1998-0.7-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR PILING DATE: 1998-0.7-02
PRIOR FILING DATE: 1998-0.7-02
PRIOR FILING DATE: 1998-0.7-02
PRIOR PILING DATE: 1998-0.7-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR PILING DATE: 1998-0.7-02
PRIOR PELING DATE: 1998-0.7-07
PRIOR PILING DATE: 1998-0.7-07
PRIOR PILING DATE: 1998-0.7-07
PRIOR PILING DATE: 1998-0.7-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR PILING DATE: 1998-0.7-07
PRIOR PILING DATE: 1998-0.7-07
PRIOR PILING DATE: 1998-0.7-07
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Patent No. 6956108
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Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
Napier, Mary A.
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Williams, P. Mickey
Wood, William I.
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Roy, Margaret Ann
Stewart, Timothy A.
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Fong, Sherman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Desnoyers, Luc
Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumas, Daniel
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APPLICANT:
APPLICANT:
APPLICANT:
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R APPLICATION NUMBER: 60/088655
R FILING DATE: 1998-06-09
R APPLICATION NUMBER: 60/088334
R PILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088738
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088742
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088742
R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088026
R FILING DATE: 1998-06-04
A PPLICATION NUMBER: 60/088028
R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088029
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PRICIS APPLICATION NUMBER: 60/08558

PRICIS APPLICATION NUMBER: 60/08563

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PRICIS APPLICATION NUMBER: 60/08901

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PRICIS APPLICATION NUMBER: 60/08902

PRICIS APPLICATION NUMBER: 60/08902

PRICIS APPLICATION NUMBER: 60/08903

PRICIS APPLICATION NUMBER: 60/08003

PRICIS APPL
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j Sequence 7800, Application US/09949016
j Patent No. 681239
j GENERAL INFORMATION:
j PAPLICANT: VENTER, J. Craig et al.
j TITLE OF.INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF.INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
j TITLE OF INVENTION: US/09/949,016
j FILE REFERENCE: CL001307
j CURRENT APPLICATION NUMBER: 60/241,755
j PRIOR APPLICATION NUMBER: 60/241,755
j PRIOR FILING DATE: 2000-10-20
j PRIOR FILING DATE: 2000-10-03
j PRIOR FILING DATE: 2000-10-03
j PRIOR FILING DATE: 2000-09-08
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; Batent No. 6861409;
; Batent No. 6861409;
; Charlant No. 6861409;
; GENERAL INFORMATION:
; APPLICANT: Zentaris AG
; TITLE REFERENCE: 97264-100;
; CURRENT APPLICATION NUMBER: US/09/880,498
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US Provisional Appln No. 6861409 60/231,326
; PRIOR PILING DATE: 2000-09-26
; PRIOR FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 28
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Best Local Similarity 76.2%; Pred. No. 0.0081;
Matches 16; Conservative 0; Mismatches 5; Indels
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR PLING DATE: 1998-07-02
PRIOR PLING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-07
PRIOR PELING DATE: 1998-07-07
PRIOR PLING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR APPLICATION NUMBER: 60/091982
PRIOR APPLICATION NUMBER: 60/092182
PRIOR PLING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
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LOCATION: (3) ...(3)
COTHER INFORMATION: 0-n-octanoyl
US-09-880-498-1
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ORGANISM: rat
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US-09-880-498-1
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US-09-902-540-13645
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT FILING DATE: 1999-02-18

PRIOR PILING DATE: 1999-02-18

PRIOR PELING DATE: 1998-02-18

PRIOR PILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 569
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                                                                                                                                                                                                                                                                                           45 H-----VVPALPLSNQLCDLEQQRHLWASVFSQSTKDSGSDLTVSGRTWGLRVLNRLF 97
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REPERENCE: 38-10 (15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
                                                                                                                                                                                                                                                                  ---LLLLGMLWLDLAMAGS---SFLSPEHQRVQVRP-PHKAP
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31.3%; Pred. No. 2.2;
tive 9; Mismatches 34; Indels 25; Gaps
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                       40;
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NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREUSEQ for Windows Version 4.0
SEQ ID NO 7800
LENGTH: 597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27248
                                                                                                                                                         Query Match
Best Local Similarity 27.4%,
"...Asg 34; Conservative
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Best Local Similarity 31.3'
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US-09-902-540-13645
                                                                                    ; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7800
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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions .rnpbm (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions .rapbm (Published_Applications_AA_Main) and .rapbn (Published_Applications_AA_New).

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101, App 196, App 23, Appl 23, Appl 17, Appl 117, Appl 141, Appl 1560, Ap 276, Ap 276, Ap 276, Ap 276, Ap 112, Appl 28, Appl 28, Appl 28, Appl 28, Appl 28, Appl 29, Appl 210, A

Sequence Seq

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APPLICANT: BARES, KRVIN F.

APPLICANT: BARES, KRVIN F.

APPLICANT: BERCEGE, Laura
APPLICANT: DeFOGES, Laura
APPLICANT: DeFOGES, Laura
APPLICANT: Good-Gerit Gen.
APPLICANT: Smith, Victoria
APPLICANT: Matanabe, Colin K
APPLICANTON NUMBER: 60/05911
RRIOR APPLICANTON NUMBER: 60/05911
RRIOR PLILING DATE: 1997-09-17
RRIOR RAPLICANTON NUMBER: 60/05912
RRIOR RAPLICANTON NUMBER: 60/05912
RRIOR RAPLICANTON NUMBER: 60/05913
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                                 US-11.186-284-101

US-10-485-517-196

US-11-080-991-104

US-11-093-746A-23

US-11-108-528-82

US-11-108-528-82

US-11-108-528-141

US-10-467-657-550

US-11-186-284-141

US-10-467-657-1560

US-11-102-978-2

US-11-002-978-2

US-11-002-978-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 442, Application US/10131826A Publication No. US20050245730A1 GENERAL INFORMATION: APPLICANT: Baker, Kevin P.
  155
193
3193
3193
3193
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101
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    RESULT 1
US-10-131-826A-442
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                                                                                                                                        December 21, 2005, 13:32:53 ; Search time 12 Seconds (without alignments) 69.538 Million cell updates/sec
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1 MPSPGTVCSLLLLGMLWLDL......PPSSRERSRRSHQPSCSPEL 117
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Sequence 4
Sequence 5
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/cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
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                        GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-11-186-294-1368
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US-11-108-528-84
US-11-108-528-86
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US-11-087-084-30
US-11-087-084-6
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US-11-087-083-6
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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RESULT 5
US-11-108-528-84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Labar, Ivan
APPLICANT: Labar, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
ITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE KEFERNCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ_genes Version 1.0
SEQ ID NO 1368
LENGTH: 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 CMLWLDLAMAGSSFLSPEHQRVQVRPPHKAPHVVPALPLSNQ---LCDLEQQRHLWASVF 70
                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                 Score 198; DB 6; Length 117;
Pred. No. 4.4e-16;
0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                               1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHORVQVRPPHKAP 44
                                                                                                                                                                                                                                                                                             1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 ESAARENGNPGQIAGST-GL----LFNLPPGS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 SQSTKDSGSDLTVSGRTWGLRVLNRLF--PPSS 101
                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 1368, Application US/10821234; Publication No. US20050255114A1; GENERAL INFORMATION;
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                                                                                                                                                                 Query Match
Best Local Similarity 88.6%;
Matches 39; Conservative C
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 442
LENGTH: 117
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                                                                                              ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 28; Conserv
                                                                                                                       US-10-131-826A-442
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APPLICANT: Jacobs, Kenneth
APPLICANT: Jacobs, Kenneth
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M
APPLICANT: Racie, Lisa A
APPLICANT: Racie, Lisa A
APPLICANT: Evans, Cheryl
APPLICANT: Tracy, David
APPLICANT: Tracy, Murrice
APPLICANT: Tracy, Murrice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE OF INVENTION SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING
FILE REFERENCE: 00766, 0000991.10
CURRENT APPLICATION NUMBER: US/10/689,742
CURRENT APPLICATION NUMBER: 09/746,783
PRIOR APPLICATION NUMBER: 09/746,783
PRIOR PELING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 231
SOFTWARE: Patentin version 3.2
SEQ ID NO 142
LENGTH: 903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 QSTRESWVSPRKRGLSSSEKDNIERQAIENCERRQTEPVSPVLKRI-----KRCLRSEA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 VGLNGLDESFCGRTLRNRSIAHPEEISSNSOVRSRSPKKRPEPVPIQKGNNNGRTTDLKQ 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 LGMLWLDLAMAG----SSFLSPE----HQRVQVRPPHKAPHVVPALPLSN--QLCDLEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43 APHVVPALPLSN-----QLCDLEQQRHL----WASVFSQSTKDSGSDLTV 83
                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                              Score 63; DB 7; Length 303;
Pred. No. 3.9;
9; Mismatches 18; Indel8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36; Conservative 16; Mismatches
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR PELING DATE: 2001-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR PILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SEQ ID NO 193
LENGTH: 303
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Publication No. US20050250180A1
GENERAL INFORMATION:
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Publication No. US20050261189A1
GENERAL INFORMATION:
APPLICANT: Larsen, Glenn
                                                                                                                                                                                                                                                                                                                                                                                       Query Match 10.2%;
Best Local Similarity 27.5%;
Matches 14; Conservative 9
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ORGANISM: Homo sapiens
US-10-689-742-142
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US-11-186-284-193
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Best Local Similarity
Matches 36; Conserva
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128 PNSSEE 133
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179 PPQRSLCSSDFIRILVIFSGMFLVFTLAGALFL---HQRRKYRSNKGESPVEPAEPCR-- 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 HKAPHVVPALPLSNQLCDLEQQRHLWASVPSQSTKDSGSDLTVSGRTWGLRVLNRLFPPS 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 PSPGTVCS-----LLLLGMLWLDLAWAGSSFLSPEHQRVQVRPPHKAPHVVPALPLSNQ 55
                                                                                                                                                                                                                                                                                                                                                                        28; Gaps
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9.8%; Score 61; DB 7; Length 260;
Best Local Similarity 20.8%; Pred. No. 5.5;
Matches 25; Conservative 17; Mismatches 34; Indela
                                                                                                                                                                                                                Query Match
9.8%; Score 61; DB 7; Length 96;
Best Local Similarity 26.3%; Pred. No. 1.7;
Matches 20; Conservative 7; Mismatches 21; Indels
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APPLICANT: Wei, Ying-Fei
APPLICANT: Wei, Ying-Fei
APPLICANT: Wei, Ying-Fei
APPLICANT: Roler, Reiner
APPLICANT: Ruben, Steven
TITLE OF INVENTION: Tumon Necrosis Factor Receptor 5
FILE REFERENCE: 1488 1280004
CURRENT APPLICATION NUMBER: US/11/182,946
CURRENT APPLICATION NUMBER: US/21/186,643
PRIOR APPLICATION NUMBER: US/209/573,986
PRIOR APPLICATION NUMBER: US/209/573,986
PRIOR FILING DATE: 2002-07-18
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 260
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Publication No. US20050276814A1
GENERAL INFORMATION:
APPLICANT: Microbial Technics Limited
APPLICANT: Gilbert, Christophe FG
APPLICANT: Hansbro, Philip M
TILLE OF INVENTION: Proteins
FILE REFERENCE: PWC/P21129W0
CURRENT APPLICATION NUMBER: US/10/873,528
CURRENT FILING DATE: 2004-06-23
PRIOR FILING DATE: 2004-06-23
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 944
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 931
LENGTH: 96
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Publication No. US20050255100A1
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CRGANISM: Homo sapiens
US-11-182-946-8
                                                                                                               TYPE: PRT
CORGANISM: Homo sapiens
US-11-000-463-931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 DLEQORHLWASVFSQSTKDSGSDLTVSGRTWGLRVLNRLFPPSSRERSR----RSHQPSC 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 PSPGTVCSLLLLGMLWLDLAMAGSSFLSPE-HORVOVRP---PHKAPHVVPALPLSNQLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1613;
                            APPLICANT: ii, Dean Y.
APPLICANT: Wang, Elizabeth
APPLICANT: Wang, Elizabeth
APPLICANT: Chen, C. M. AMM.
TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
TITLE OF INVENTION: PROLIFERATION
FILE REFERENCE: HYDR-PO1-041
CURRENT APPLICATION NUMBER: US/11/108,528
CURRENT FILING DATE: 2005-04-18
PRIOR PELING DATE: 2004-04-16
PRIOR APPLICATION NUMBER: US 60/598,368
PRIOR FILING DATE: 2004-04-16
PRIOR APPLICATION NUMBER: US 60/598,368
PRIOR FILING DATE: 2004-04-16
SRIGHE OF SEQ ID NOS: 86
SOFTWARE: FARSEEQ for Windows Version 4.0
SEQ ID NO 84
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APPLICANT: Zhou, Ping
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 785CIP4CN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 7;
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CURRENT APPLICATION NUMBER: US/11/000,463
CURRENT FILING DATE: 2004-11-29
PRIOR APPLICATION NUMBER: US/21,265
PRIOR FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR PILING DATE: 2001-01-25
PRIOR PLING DATE: 2001-01-25
PRIOR FILING DATE: 2000-03-25
PRIOR FILING DATE: 2000-07-17
PRIOR PELING DATE: 2000-07-17
PRIOR PELING DATE: 2000-07-17
PRIOR PELING DATE: 2000-07-17
PRIOR PELING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
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; Sequence 931, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Chen, Rui-hong
APPLICANT: Qian, Xiaohong B.
APPLICANT: Wang, Zhiwei
APPLICANT: Wehrman, Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 27.9%
Matches 34; Conservative
           Marvin, Martha
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1588 PP 1589
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ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 LGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAPHVVPALPLSNQLCDLEQQRHLWASVFSQ 72
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9.6%; Score 59.5; DB 7; Length 1615;
Best Local Similarity 25.0%; Pred. No. 72;
Matches 30; Conservative 14; Mismatches 41; Indels 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 9.6%; Score 59.5; DB 6; Length 465; Best Local Similarity 24.7%; Pred. No. 16; Astches 23; Conservative 13; Mismatches 38; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:

APPLICANT: Largen, Glenn
APPLICANT: Li, Dean Y.
APPLICANT: Li, Dean Y.
APPLICANT: Wang, Elizabeth
APPLICANT: Chen, C. M. Amy
APPLICANT: Shamah, Steven M.
TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
TITLE OF INVENTION: PROLIFERATION
TITLE REFERENCE: HYDR-POl.041
CURRENT APPLICATION NUMBER: US/11/108,528
CURRENT FILING DATE: 2004-04-16
PRIOR APPLICATION NUMBER: US 60/598,368
PRIOR PILLING DATE: 2004-04-16
PRIOR PELLING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 86
SOFTWARE: FastESQ for Windows Version 4.0
SEQ ID NO 80
LENGTH 1615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    || : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | |: |: || || || 5 PISDNSSEVIVQPRIVETIVKD---PSSTARET 84
PRIOR APPLICATION NUMBER; GB 9816337.1 PRIOR FILING DATE: 1998-03-27 PRIOR APPLICATION NUMBER; US 60/125164 PRIOR FILING DATE: 1999-03-19 NUMBER OF SEQ ID NOS: 388 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 164
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Publication No. US20050261189A1
GENERAL INFORMATION:
APPLICANT: Larsen, Glenn
APPLICANT: Marvin, Martha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 80, Application US/11108528 Publication No. US20050261189A1 GENERAL INFORMATION:
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1538 D------SDYAPSRRMT-SVATAKGYTSDVNYDSEPVPPPPTPRSQYLSAEENYESC 1587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 DLEQQRHLWASVFSQSTKDSGSDLTVSGRTWGLRVLNRLFPPSSRERSR----RSHQPSC 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 PSPGTVCSLLLLGMLWLDLAMAGSSFLSPE-HQRVQVRP---PHKAPHVVPALPLSNQLC
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9.4%; Score 58.5; DB 7; Length 1613;
Best Local Similarity 27.0%; Pred. No. 94;
Matches 33; Conservative
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APPLICANT: Li, Dean Y.
APPLICANT: Wang, Elizabeth
APPLICANT: Chen, C. M. Amy
APPLICANT: Chen, C. M. Amy
APPLICANT: Steven M.
TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
TITLE OF INVENTION: PROLIFERATION
FILE REFERENCE: HYDR-Pol-04 US/11/108,528
CURRENT APPLICATION NUMBER: US/11/108,528
CURRENT FILING DATE: 2005-04-18
PRIOR FILING DATE: 2004-04-16
PRIOR FILING DATE: 2004-04-16
PRIOR FILING DATE: 2004-04-16
PRIOR FILING DATE: 2004-04-16
SRIOR PRIOR FILING DATE: 2004-04-16
SRIOR FILING DATE: 2004-04-16
SRIOR FILING DATE: 2008-08-02
NUMBER OF SEQ ID NOS: 86
SOFTWARE: FEASTEED for Windows Version 4.0
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APPLICANT: Murdock, Paul R.
APPLICANT: Murdock, Paul R.
APPLICANT: Smith, Randall F.
APPLICANT: Smith, Randall F.
APPLICANT: Sinth, Randall F.
APPLICANT: NAME, 2005-06-07
FILE OF INVENTION NUMBER: US/10/221,097
FRIOR PILING DATE: 2005-06-07
FRIOR APPLICATION NUMBER: PCT/USO1/07143
FRIOR FILING DATE: 2001-03-05
FRIOR PILING DATE: 2001-03-05
FRIOR PILING DATE: 2000-10-03
FRIOR PILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
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GENERAL INCORPAIL TOWN:

GENERAL INCORPAIL TOWN:

APPLICANT: Barclay, William

APPLICANT: Flatt, James

APPLICANT: Flatt, James

APPLICANT: Flatt, James

APPLICANT: Roner, Jerry

TITLE OF INVENTION: Nucleic Acid Molecule Encoding ORFA of a PUFA Polyketide Synthase

TITLE OF INVENTION: System and Uses Thereof

TITLE OF INVENTION: System and Uses Thereof

TITLE OF INVENTION: System and Uses Thereof

CURRENT APPLICATION NUMBER: 09/231, 899

PRIOR FILING DATE: 2005-03-21

PRIOR FILING DATE: 2001-04-16

PRIOR FILING DATE: 2001-04-16

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-18

NUMBER OF SEQ ID NOS: 37

SOFTWARE: PatentIN VERSION 3.3

SEQ ID NO 30

LENGTH: 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 395 WFDSVMPGSLGVESMFOLVEALAAHEDLAGKARHCOP-----HLCARPRARSSWKYRGQ 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 57.5, DB Pred. No. 30; 4; Mismatches
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I Similarity 25.3%; Pred. No. 30;
25; Conservative 4; Mismatches
PRIOR FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: 60/298,796
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/323,269
PRIOR FILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PATCHIN Version 3.3
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; Publication No. US20050273884A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 30, Application US/11087084
Publication No. US20050273883A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.3%;
                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Schizochytrium sp.
US-11-087-100-30
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ORGANISM: Schizochytrium sp.
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US-11-087-085-30
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APPLICANT: Barclay, William
APPLICANT: Runer, Jerry
TITLE OF INVENTION: Nucleic Acid Molecule Encoding ORFA of a PUFA Polyketide Synthase
TITLE OF INVENTION: System and Uses Thereof
TITLE OF INVENTION NUMBER: US/11/087,100
CURRENT APPLICATION NUMBER: US/21,899
PRIOR FILING DATE: 1999-01-14
PRIOR FILING DATE: 1999-01-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Labar, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Susan
APPLICANT: Tang, Y. Ton
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR PILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: PE_SEQ_genes Version 1.0
SEQ ID NO 1283
LENGTH: 1627
                                                                                                                                                                                                                                                                                                                     707 GSACHLCLEGRILVOYASNASPMPCSPSGHWSPREAEGHPDVEOPCKSSVRTWSPNSAV 766
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                                                                                                                                                                                                 82
                                                                                                                                                                                                                                                                           41 ---HKAPHVVPALPLSNQLCDLEQQRH-----LWASVFSQSTKDSGSDLTVSG--RTW 88
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                                                                                                                        5 GTVCSLLLLGMLWLDLA----MAGSSFLSPEHQRVQVRPP-----
                                                      42; Indels
                   Best Local Similarity 20.5%; Pred. No. 12; Matches 30; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  89 GLRVLNRLFPPSSRERSRRSHQPSCS 114
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|34. RLRLISR-------PTCN 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 GTVCSLLLLGMLWLDLAMAGSSFL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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US-11-087-100-30
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Gaps

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GENERAL INFORMATION:
APPLICANT: Metz, James
APPLICANT: Barclay, William
APPLICANT: Barclay, William
APPLICANT: Flatt, James
APPLICANT: Flatt, James
TITLE OF INVENTION: Nucleic Acid Molecule Encoding ORFA of a PUFA Polyketide Synthase
TITLE OF INVENTION: System and Uses Thereof
TITLE OF INVENTION: System and Uses Thereof
TITLE OF INVENTION: System and Uses Thereof
FILE REFERENCE: 2997-29
CURRENT APPLICATION NUMBER: US/11/087,085
CURRENT FILING DATE: 2005-03-21,
PRIOR FILING DATE: 2001-04-16
PRIOR FILING DATE: 2001-04-16
PRIOR FILING DATE: 2001-04-16
PRIOR FILING DATE: 2001-04-16
PRIOR FILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 37
SEQ ID NO 30
LENGTH: 500
LENGTH: 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
9.3%; Score 57.5; DB 7; Length 500;
Best Local Similarity 25.3%; Pred. No. 30;
Matches 25; Conservative 4; Mismatches 41; Indels 29; Gaps
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; ORGANISM: Schizochytrium sp.
US-11-087-085-30
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Search completed: December 21, 2005, 13:41:46 Job time : 13 Bec8